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GTCGACCCACGCGTCCGCGCCACGCGTCCGCGCC	ATG	GCG	CCG	CCC	GCC	GCC	GCC	CTC	CTC	GCC	CTG	CTC	11
	M	A	P	P	A	A	R	L	A	L	L		66
S	A	A	A	L	T	L	A	A	R	P	A	P	31
TCC	GCC	GCG	GCG	CTC	ACG	CTG	GCG	GCC	CGG	CCT	AGC	CCC	126
	P	E	C	F	T	A	N	G	A	D	Y	R	51
CCC	GAG	TGT	TTC	ACA	GCC	AAT	GGT	GCG	GAT	TAT	AGG	GGA	186
	Q	G	G	K	P	C	L	F	W	N	E	T	71
CAA	GGC	GGG	AAG	CCA	TGT	CTG	TTT	TGG	AAC	GAG	ACT	TTC	246
	K	Y	P	N	G	E	G	L	G	E	H	N	91
AAA	TAC	CCC	AAC	GGG	GAG	GGG	CTG	GGT	GAG	CAC	AAC	TAT	306
	D	V	S	P	W	C	Y	V	A	E	H	E	111
GAC	GTG	AGC	CCC	TGG	TGC	TAT	GTG	GCA	GAG	CAC	GAG	GAT	366
	E	I	P	A	C	Q	M	P	G	N	L	G	131
GAG	ATA	CCT	GCT	TGC	TGC	CAG	ATG	CCT	GGA	AAC	CTT	GGC	426
	P	P	L	T	G	T	S	K	T	S	N	K	151
CCT	CCT	CTA	ACT	GGC	ACC	AGT	AAA	ACG	TCC	AAC	AAA	CTC	486
	F	C	R	S	Q	R	F	K	F	A	G	M	171
TTT	TGT	CGG	AGT	CAG	AGG	TTC	AAG	TTT	GCT	GGG	ATG	GAG	546

Fig. 1A

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G	N	N	P	D	Y	W	K	Y	G	E	A	A	S	T	E	C	N	S	V	191
GGA	AAC	AAT	CCT	GAT	TAC	TGG	AAG	TAC	GGG	GAG	GCA	GCC	AGT	ACC	GAA	TGC	AAC	AGC	GTC	606
C	F	G	D	H	T	Q	P	C	G	G	D	G	R	I	I	L	F	D	T	211
TGC	TTC	GGG	GAT	CAC	ACC	CAA	CCC	TGT	GGT	GGC	GAT	GGC	AGG	ATC	ATC	CTC	TTT	GAT	ACT	666
L	V	G	A	C	G	G	N	Y	S	A	M	S	S	V	V	Y	S	P	D	231
CTC	GTG	GGC	GCC	TGC	GGT	GGG	AAC	TAC	TCA	GCC	ATG	TCT	TCT	GTG	GTC	TAT	TCC	CCT	GAC	726
F	P	D	T	Y	A	T	G	R	V	C	Y	W	T	I	R	V	P	G	A	251
TTC	CCC	GAC	ACC	TAT	GCC	ACG	GGG	AGG	GTC	TGC	TAC	TGG	ACC	ATC	CGG	GTT	CCG	GGG	GCC	786
S	H	I	H	F	S	F	P	L	F	D	I	R	D	S	A	D	M	V	E	271
TCC	CAC	ATC	CAC	TTC	AGC	TTC	CCC	CTA	TTT	GAC	ATC	AGG	GAC	TCG	GCG	GAC	ATG	GTG	GAG	846
L	L	D	G	Y	T	H	R	V	L	A	R	F	H	G	R	S	R	P	P	291
CTT	CTG	GAT	GGC	TAC	ACC	CAC	CGT	GTC	CTA	GCC	CGC	TTC	CAC	GGG	AGG	AGC	CGC	CCA	CCT	906
L	S	F	N	V	S	L	D	F	V	I	L	Y	F	F	S	D	R	I	N	311
CTG	TCC	TTC	AAC	GTC	TCT	CTG	GAC	TTC	GTC	ATC	TTG	TAT	TTC	TTC	TCT	GAT	CGC	ATC	AAT	966
Q	A	Q	G	F	A	V	L	Y	Q	A	V	K	E	E	L	P	Q	E	R	331
CAG	GCC	CAG	GGA	TTT	GCT	GTT	TTA	TAC	CAA	GCC	GTC	AAG	GAA	GAA	CTG	CCA	CAG	GAG	AGG	1026

Fig. 1B

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P	A	V	N	Q	CAG	ACG	GTG	GCC	GAG	GTG	ATC	ACG	GAG	Q	A	N	L	S	V	S	351	
CCC	GCT	GTC	AAC	CAG	CAG	ACG	GTG	GCC	GAG	GTG	ATC	ACG	GAG	Q	A	N	L	S	V	S	1086	
A	A	R	S	S	TCC	TCC	AAA	GTC	TAT	GTC	ATC	ACC	ACC	T	S	P	S	H	P	P	Q	371
GCT	GCC	CGG	TCC	TCC	TCC	AAA	GTC	CTC	TAT	GTC	ATC	ACC	ACC	T	S	P	S	H	P	P	Q	1146
T	V	P	G	S	GGT	AGC	AAT	TCC	TGG	GCG	CCA	CCC	ATG	GGG	GCT	GGA	AGC	CAC	AGA	GTT	GAA	391
ACT	GTC	CCA	GGT	AGC	AAT	TCC	TGG	GCG	CCA	CCC	ATG	GGG	GCT	GGA	AGC	CAC	AGA	GTT	GAA	GTT	GAA	1206
G	W	T	V	Y	G	L	A	T	A	T	L	I	L	T	V	T	A	I	V	A	A	411
GGA	TGG	ACA	GTC	TAT	GGT	CTG	GCA	ACT	CTC	CTC	ATC	CTC	ACA	GTC	ACA	GCC	ATT	GTA	GCA	GTA	GCA	1266
K	I	L	L	H	V	T	F	K	S	H	R	V	P	A	S	G	D	L	R	A	R	431
AAG	ATA	CTT	CTG	CAC	GTC	ACA	TTC	AAA	TCC	CAT	CGT	GTT	CCT	GCT	TCA	GGG	GAC	CTT	AGG	CTT	AGG	1326
D	C	H	Q	P	G	T	S	G	E	I	W	S	I	F	Y	K	P	S	S	T	T	451
GAT	TGT	CAT	CAA	CCA	GGG	ACT	TCG	GGG	GAA	ATC	TGG	AGC	ATT	TTT	TAC	AAG	CCT	TCC	ACT	TCC	ACT	1386
S	I	S	I	F	K	K	K	L	K	G	Q	S	Q	Q	D	D	R	N	P	P	P	471
TCA	ATT	TCC	ATC	TTT	AAG	AAG	AAA	CTC	AAG	GGT	CAG	AGT	CAA	CAA	GAT	GAC	CGC	AAT	CCC	CCC	CCC	1446
L	V	S	D	*																		476
CTT	GTG	AGT	GAC	TAA																		1461

Fig. 1C

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AAACCCACTGTGCCCTAGGACTTGAAGTCCCTCTTTGAGCTCAAGGCTGCCGTGGTCAACCTCTCCTGTGGTTCTTCTC 1540  
TGACAGACTTTCCTCCTCTCCCTCTGCTCGGCTCTTTCGGGAAACCTCCTCCTACAGACTAGGAAGAGGCACCT 1620  
GCTGCCAGGCAGGCAGGCTGGATTCCCTCCTGCTT 1657

Fig. 1D

GTCGACCCACGCGTCCGCCCGGCTCCCGGTGCTGCCCTCTGCCCCGGCGCGCGGGGTCCCCGCACTGACGGCC 79

M A P P A A R L A L L S A A A L T L A 19  
C ATG GCG CCG CCC GCC GCC CGT CTC GCG CTG CTC TCC GCC GCT GCG CTC ACT CTG GCG 137

A R P A P G P R S G P E C F T A N G A D 39  
GCC CGG CCC GCG CCC GGT CCC CGC TCC GGC CCC GAG TGC TTC ACA GCC AAC GGT GCA GAT 197

Y R G T Q S W T A L Q G G K P C L F W N 59  
TAC AGG GGA ACA CAG AGC TGG ACA GCG CTG CAA GGT GGG AAG CCA TGT CTG TTC TGG AAC 257

E T F Q H P Y N T L K Y P N G E G L G 79  
GAG ACT TTC CAG CAT CCG TAC AAC ACG CTG AAG TAC CCC AAC GGG GAA GGA CTG GGC 317

E H N Y C R N P D G D V S P W C Y V A E 99  
GAG CAC AAT TAT TGC AGA AAT CCA GAT GGA GAC GTG AGC CCT TGG TGC TAC GTG GCC GAG 377

Fig.1E



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H	E	D	G	G	V	Y	W	K	Y	C	E	I	P	A	C	Q	M	P	G	N	119
CAT	GAG	GAC	GGA	GTC	TAC	TGG	AAG	TAC	TGT	GAA	ATT	CCT	GCC	TGC	CAG	ATG	CCT	GGA	AAC	437	
L	G	C	Y	K	D	H	G	N	P	P	P	L	T	G	T	S	K	T	S	139	
CTT	GGC	TGC	TAC	AAG	GAT	CAT	GGA	AAC	CCA	CCT	CCT	CTC	ACG	GGC	ACC	AGT	AAA	ACC	TCT	497	
N	K	L	T	I	Q	T	C	I	S	F	C	R	S	Q	R	F	K	F	A	159	
AAC	AAG	CTC	ACC	ATA	CAA	ACC	TGT	ATC	AGC	TTC	TGT	CGG	AGT	CAG	AGA	TTC	AAG	TTT	GCT	557	
G	M	E	S	G	Y	A	C	F	C	G	N	P	D	Y	W	K	H	G	G	179	
GGG	ATG	GAG	TCA	GGC	TAT	GCC	TGC	TTC	TGT	GGG	AAC	AAT	CCT	GAC	TAC	TGG	AAG	CAC	GGG	617	
E	A	A	S	T	E	C	N	S	V	C	F	G	D	H	T	Q	P	C	G	199	
GAG	GCG	GCC	AGC	ACC	GAG	TGC	AAT	AGT	GTC	TGC	TTC	GGG	GAC	CAC	ACG	CAG	CCC	TGC	GGT	677	
G	D	G	R	I	I	L	F	D	T	L	V	G	A	C	G	G	N	Y	S	219	
GGG	GAC	GGC	AGG	ATT	ATC	CTC	TTT	GAC	ACT	CTC	GTG	GGC	GCC	TGC	GGT	GGG	AAC	TAC	TCA	737	
A	M	A	A	V	V	Y	S	P	D	F	P	D	T	Y	A	T	G	R	V	239	
GCC	ATG	GCA	GCC	GTG	GTG	TAC	TCC	CCT	GAC	TTC	CCT	GAC	ACC	TAC	GCC	ACT	GGC	AGA	GTC	797	
C	Y	W	T	I	R	V	P	G	A	S	R	I	H	F	N	F	T	L	F	259	
TGC	TAC	TGG	ACC	ATC	CGG	GTT	CCA	GGA	GCC	TCT	CGC	ATC	CAT	TTC	AAC	TTC	ACC	CTG	TTT	857	
D	I	R	D	S	A	D	M	V	E	L	L	D	G	Y	T	H	R	V	L	279	
GAT	ATC	AGG	GAC	TCT	GCA	GAC	ATG	GTG	GAG	CTG	CTG	GAC	GGC	TAC	ACC	CAC	CGC	GTC	CTG	917	

Fig.1F

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V R L S G R S R P P L S F N V S L D F V 299  
 GTC CGG CTC AGT GGG AGG AGC CGC CCT CTG TCT TTC AAT GTC TCT TCT GAT TTT GTC 977  
  
 I L Y F F S D R I N Q A Q G F A V L Y Q 319  
 ATT TTG TAT TTC TTC ATC GAT CGC ATC AAT CAG GCC CAG GGA TTT GCT GTG TTG TAC CAA 1037  
  
 A T K E E P P Q E R P A V N Q T L A E V 339  
 GCC ACC AAG GAG GAA CCG CCA CAG GAG AGA CCT GCT GTC AAC CAG ACC CTG GCA GAG GTG 1097  
  
 I T E Q A N L S V S A A H S S K V L Y V 359  
 ATC ACC GAG CAA GCC AAC CTC AGT GTC AGC GCT GCC CAC TCC TCC AAA GTC CTC TAT GTC 1157  
  
 I T P S P S H P P Q T A Q V A I P G H R 379  
 ATC ACC CCC AGC CCC AGC CAC CCT CCG CAG ACT GCC CAG GTA GCC ATT CCT GGG CAC CGT 1217  
  
 Q L G P T A T E W K D G L C T A W R P S 399  
 CAG TTG GGG CCA ACA GCC ACA GAG TGG AAG GAT GGA CTG TGT ACG GCC TGG CGA CCC TCC 1277  
  
 S S S Q S Q Q L S Q R F F C M S H L N L 419  
 TCA TCC TCA CAG TCA CAG CAG TTG TCG CAA AGA TTC TTC TGC ATG TCA CAT TTA AAT CTC 1337  
  
 I E S L H Q E T L G T V S L G L L E I 439  
 ATC GAG TCC CTG CAT CAG GAG ACC TTA GGG ACT GTC AGC CTG GGG CTT CTG GAG ATA 1397  
  
 S G P F S M N L P L Q S P S L R S S R 459  
 TCT GGA CCA TTT TCT ATG AAC CTT CCA CTA CAA TCT CCA TCT TTA AGA AGA AGC TCA AGG 1457

Fig.1G

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V R V N K M T A I P S \*  
GTC AGA GTC AAC AAG ATG ACC GCA ATC CCC TCG TGA 471 1493

GTGACTGAAGCCACGCCCTGCATGAGAGGCTCCGCTCCAAAGCTCGAGTTTGCTCCCCCTGAGTTCTCCTCTGATGAGTTC 1572  
CCTGCCCTTCCCATTCACCAACCATCTCTTTTGGAGCACCCCTGCTTTAGAGGCAGCCAGCTGGATCCTCCATCACAT 1651  
GTACCAGCCTGGCTGCTCTGCTGGGATGTTAAGACAGGCCAGGCTGACAGGACACAGCTGGACCTGACTCCAGAAGA 1730  
CTCTTGGGTGGGAGGTATAGTGTAGGATGAGTTTCTTGTCTCTCTGTTTGTCCACATACAGATCGGTTTC 1809  
CCCTGTCTTTACAGTTTGCAATAGAGCCAGACTGAAAGAACTGTACAGTTTCTAGGCTGGCCTGGTTCCTCCACTAAGA 1888  
GTGGCATTTGGCCCCCTAGAGGCCACAGAGGCCAGTGTAGGCTTTGGAGCTTTCTCTGCTGCCAACTACCATGTGTCATCT 1967  
AGTCCGAGGGACTGAGAGCAGGGCCACACAGATGTCACTTTCTAGAGGGTTCTTTTAGTACCCACTGACCCAATGG 2046  
GGCAAGCCTGAGGATTGGTCCATCTGTTTGTCCATGGAACACAGACAGTGAACCTCCCTGGATACAGACTTAAGTACC 2125  
TAGCCCTCAAGTAGTTGCCAATCCTGTGGAAATCAGAAATTCAGCCTGTCTTCTGTCCAGCCCCAAGCCTGTAGCCTAG 2204  
AGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCACAGAGCTGGGGCTGTAGCCTAGAGC 2283  
TGGGGCTGTAGCACAGAGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCACAGAGCTGGGGCTGTAGCACAGAGCTGG 2362  
GGCTGTAGCCTAGAGCTGGGGCTGTAGCACAGAGCTGGGGCTGTAACTCAGCGATCAAGAGCTTGCTTTGTATACATCG 2441  
GACCTAGGTTCTATCCAGCACTATCAGAAAGGTGGGAGAGAAAGACTGCACATAGCATGCGGGCAGCATCTGTGG 2520  
TTCCCTACGTGAGGTGTCATCATTTTAAAGCAGATCAAAACTACCGGAGTTTGTCTCTTTGTCCCTTATCATGGGAGC 2599  
AGAGTAGGAGTAAGGGCTCTGGTCTTGTCTATTGTCTCCAGACAGGAGGAGGAGGAAAGGTCAAGCTTGGGAACTGGA 2678  
GATCCTCCAGGAAAAGCTGCAAGATTGAGAGACCCAGCTGCAGTTGGGAGAGGAAGGCCATCCCCGACTGAGAAGTC 2757  
CTGCAGTCTGGAAGTGGCTTTGTACAGCAGCAGCTGTGCCCTGAAGGTAGACCTTGGTCACTCTCCTGCCAGCCCTTGA 2836  
GCCTCTGCTCTCCTGGGTACCCCTCCTGGAACACCATGCTAACCTTCCCCGAGTCTCTCAGTCACTGCCATTGAGGCCCTC 2915  
TCCCTAGCTGCTGCTCCAGGACTGTCTGGGGCCATCTGGGATCAGGAGAGGAGGAGGAGTACTGACGAGGCGAG 2994  
TGACCTGAGCTGATGAGTCAACCAGAGGACACAGAGTCTACAGTGGGCTGGCTGCTGGCTCAGCTCCTATGGGAGGCC 3073  
TACAGGGGTACTAAGCTAGGGGTGTCATCTCATTTGATCTGGGAAAGGCTACAGGCTCCTGGATGTGAAGACAGGCC 3152  
CACTACATAAGAAGACCCTGGAAATAGACTGACAGGAGCAGGTTCCACTCTAGGCTGTCCATAGCGTTTGCAGGACTC 3231

Fig.1H

CCCAGAGCAAGTGTGAGTCACAGAGTGCCATGTGCGTAGTGCAATAAGGATATGGGTTCTTAACAGGGAAGGCTC 3310  
 ATAGCAGGCCAGGACATTTTTCAGCTCAGAGCACTGGCCCCAGGCTTCCCTTAAGCCACCACCTCACCTGTCTCTTCCCT 3389  
 ATCTCGGACACAGGAAGCAAGCCCAAGTGTGGTGGCAGCTGCGGCTCAGCATTTGGTGTCCCAAGGAGGCGGTGATG 3468  
 TGGCCACGCTCCTTTTGTGTGGGCTTGCCACAGCCCAACACTGCAGGGCCACCTTCTCTCTTGGGGGTAGGGACAC 3547  
 ATAAAGGAAACTAACCCACCTCAACAACAGCAGAGGACAGTGGGAAGGAGGCTGTAAATCACCCAGGCCAGACCTC 3626  
 CAGAAATGACAGGCACAGTCTGTATTAGAACCTGTAGGCAGCCAGTCACAGAGGGCTTTGTGCTGTGTAACACCCCTGCCTG 3705  
 GAGCATAGGGGTAAAGCCGAGGAGAACAGCAGCCCTCAGAGACATCAGCTAAACATAGGTGCCCTATGTCCCTCCCT 3784  
 TCCCTGTCACACTGCTTACAAAGCAGAGACAGAGTAGGAAAGAGGTCTTCACTCTCCACATCAGCAAGGATAGGGCT 3863  
 GCGGCTGCCCTAAAGTGAGCAAGGAGAACAGAGCTCTGGACTTCTCTAAATGTGGGCTCTGGCTTCAGACTCCTCAGCCA 3942  
 AAAGCTCTTGAAATCAAGATCAAGCTCTGGGGGTACAGCTGTCTGGCTGTGGGCCAGCCCATGGGATGTCCCTGGGCCAG 4021  
 GTGCCACCCCAAGGCTCACTGTATCCAGGAGGACCCCACTGATGCTCCTCATCATCCGCTGGCCTGACACTATCA 4100  
 GAGCTCGCGCGGCTGTTCAGGGACAGACTGACTACACTTGACCTTCAAGAGCACTTAGAAGTGGATGGCCTCCAGA 4179  
 CTCTGTGAGCCCTGTGAGGGGCCACACAAGTCTCCGAGCCCAAGTCCCAAGCTCCATGGTTCCTGGCTCCTCCTCCT 4258  
 GTGGAGTGTCTTGTGATGTCTGAGGTCTGCTTTGGGTACCGCCCTGGGAACCTGCTAACCTCCGATTTGGTCCCTTTGT 4337  
 GTCTCTGTCTTACTGTCTCTTACCTCCAGGTCACTTAGCTCTGGCTGTCTGGCTGGGAGTGGGGGTGGGATGCT 4416  
 GGCTGCACCCCAAGCTGGTCTGCCAACAGAACCTGGGGCTCACACGGGCTCTCTCTCTTAGAGGGAGTGGCCGAAGTGT 4495  
 AACTGGCCCAAGCTGAGTGGGCGAGCAACAAGTGGAGGGGATCTCTCTCTTAGAGGGAGTGGCCGAAGTGT 4574  
 AGATCCAGCGAGGAGCTGCCATCCCGCCCACTTCAATAGCAGCAAGACCTTCCCATTTCCAAATCTCACCTCCAGCAG 4653  
 GGATATGACTTTGGACAACAAGGCTTTATTGTAAATATGCTCTTAAATATGCAACTTTGAGAAATAGATAGAAACATCA 4732  
 TGTATTTTAAATATAAATGAAGTGTGACACACTGTATACAAATTTAATATATATTTTGTAGGATTTTGTATTTAAGAA 4811  
 AATGGAAATGTGATGGTACTTAACTTTTACAAAAGAGAGAAAATGTTATTTTACTGTTTGAAGAAAATAAATATCTCA 4890  
 TTGTTGTAGAAAAAATAAAGGCGGCGC 4928

Fig.11

Variable	Mean	SD	Min	Max	Skewness	Kurtosis	Normality
Age	35.2	12.5	18	65	0.15	3.2	0.98
Gender	1.2	0.4	1	2	0.05	3.0	0.99
Marital Status	1.8	0.4	1	2	0.05	3.0	0.99
Education	12.5	2.5	9	16	0.15	3.2	0.98
Income	15000	5000	5000	30000	0.15	3.2	0.98
Occupation	1.5	0.5	1	3	0.05	3.0	0.99
Health Status	1.2	0.4	1	2	0.05	3.0	0.99
Stress Level	2.5	1.0	1	4	0.15	3.2	0.98
Life Satisfaction	3.5	1.0	1	5	0.15	3.2	0.98
Resilience	2.8	0.8	1	4	0.15	3.2	0.98
Optimism	3.2	0.9	1	5	0.15	3.2	0.98
Emotional Stability	2.0	0.7	1	3	0.15	3.2	0.98
Self-Esteem	3.0	0.8	1	4	0.15	3.2	0.98
Life Purpose	2.5	0.9	1	4	0.15	3.2	0.98
Gratitude	3.8	1.0	1	5	0.15	3.2	0.98
Forgiveness	3.0	0.9	1	4	0.15	3.2	0.98
Empathy	3.5	1.0	1	5	0.15	3.2	0.98
Resilience	2.8	0.8	1	4	0.15	3.2	0.98
Optimism	3.2	0.9	1	5	0.15	3.2	0.98
Emotional Stability	2.0	0.7	1	3	0.15	3.2	0.98
Self-Esteem	3.0	0.8	1	4	0.15	3.2	0.98
Life Purpose	2.5	0.9	1	4	0.15	3.2	0.98
Gratitude	3.8	1.0	1	5	0.15	3.2	0.98
Forgiveness	3.0	0.9	1	4	0.15	3.2	0.98
Empathy	3.5	1.0	1	5	0.15	3.2	0.98

Hum.	MAPPAARLALLSAAALTLAARPA	SPGLPGPECF	TANGADYRG	TQNWTALQGGKPC	CLFWNETFQHPYNT	
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	
Mur.	MAPPAARLALLSAAALTLAARPA	PGPR--SGPECF	TANGADYRG	TQSWTALQGGKPC	CLFWNETFQHPYNT	
	10	20	30	40	50	60
	80	90	100	110	120	130
Hum.	LKYPNGEGGLGEHNYCRNPDG	VDSPWCYVAEHEDGVYWKYCE	I	PACQMPGNLGCYKDHGNPP	PLTGTSKT	
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	
Mur.	LKYPNGEGGLGEHNYCRNPDG	VDSPWCYVAEHEDGVYWKYCE	I	PACQMPGNLGCYKDHGNPP	PLTGTSKT	
	70	80	90	100	110	120
						130
	150	160	170	180	190	200
Hum.	SNKLT	IQTCISFCRSQR	KFAGMESGYACFCGNNPDYWKYGEAA	STECNSVCFGDHTQPCGGD	GRIILFD	
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	
Mur.	SNKLT	IQTCISFCRSQR	KFAGMESGYACFCGNNPDYWKYGEAA	STECNSVCFGDHTQPCGGD	GRIILFD	
	140	150	160	170	180	190
						200
	220	230	240	250	260	270
Hum.	TLVGACG	GNYSAMSSVVYSPDF	PDYATGRVCYWTIRVPGASHIHESF	PLFDIRDSADMVELLDGYTHRV		
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	
Mur.	TLVGACG	GNYSAMAAVVYSPDF	PDYATGRVCYWTIRVPGASRIHFNFT	LFDIRDSADMVELLDGYTHRV		
	210	220	230	240	250	260
						270

**Fig. 1J**

TABLE 1 continued

Hum.	290	300	310	320	330	340	350
	LARFHGRSRPPLSFNVSLDFVILYFFSDRINQAQGFVLYQAVKEELPQERPAVNQTVAEVITEQANLSV						
	...	...	...	...	...	...	...
Mur.	280	290	300	310	320	330	340
	LVRLSGRSRPPLSFNVSLDFVILYFFSDRINQAQGFVLYQATKEEPPQERPAVNQTVAEVITEQANLSV						
Hum.	360	370	380	390	400	410	420
	SAARSSKVLVYVITTSPPHPPQTVPGSNSWAPPMGAGSHRVEGWTVYGLATLLILTVTAIVAKILLHVTFK						
	...	...	...	...	...	...	...
Mur.	350	360	370	380	390	400	410
	SAAHSSKVLVYVITTSPPHPPQTAQVAIPGHRQLGPTA--TEWKD-GLCTAWRPSSSSQSQQLSQRFFCM						
Hum.	430	440	450	460	470		
	SHRVPASGDLRDCHQPGTSGEIWSIFYKPKSTISIFKKKLKGQSQ-QDDRNPLVSD						
	...	...	...	...	...	...	...
Mur.	420	430	440	450	460	470	
	SHLNLIESLHQETLGTVVSLGLLEISGPFMSNLPQLQSPSLRRSSRVNVNKMTAIPS						

Fig.1K

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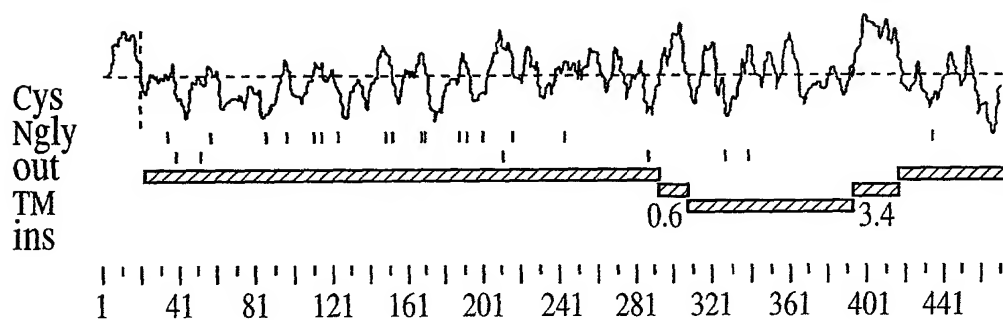


Fig. 1L

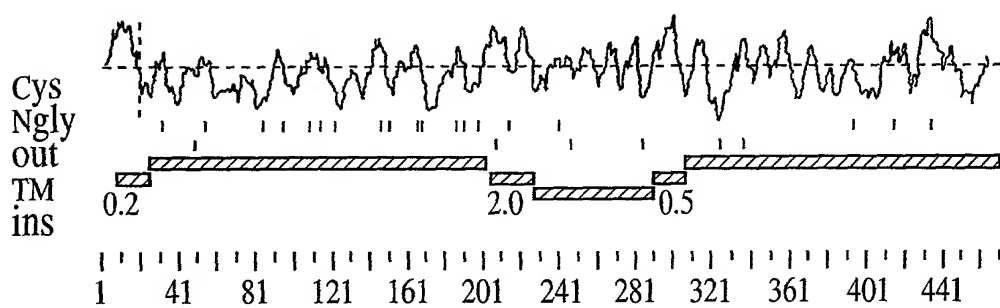


Fig. 1M

GCGGCCGCTCGGATCTAGAACTAGTA	M	M	L	P	Q	N	S	W	H	I	D	F	G	13
														66
R C C C H Q N L F S A V V T C I L L N														33
AGA TGC TGC TGT CAT CAG AAC CTT TTC TCT GCT GGT GTA ACT TGC ATC CTG CTC CTG AAT														126
S C F L I S S F N G T D L E L R L V N G														53
TCC TGC TTT CTC ATC AGC AGT TTT AAT GGA ACA GAT TTG GAG TTG AGG CTG GTC AAT GGA														186
D G P C S G T V E V K F Q G Q W G T V C														73
GAC GGT CCC TGC TCT GGG ACA GTG GAG GTG AAA TTC CAG GGA CAG TGG GGG ACT GTG TGT														246
D D G W N T A S T V V C K Q L G C P F														93
GAT GAT GGG TGG AAC ACT ACT GCC TCA ACT GTC GTG TGC AAA CAG CTT GGA TGT CCA TTT														306
S F A M F R F G Q Q A V T R H G G G A A A ATT TGG CTT GAT														113
TCT TTC GCC ATG TTT CGT TTT GGA CAA GCC GTG ACT AGA CAT GGA AAA ATT TGG CTT GAT														366
D V S C Y G N E S A L W E C Q H R E W G														133
GAT GTT TCC TGT TAT GGA AAT GAG TCA GCT CTC GCT GGT GAA TGT CAA CAC CGG GAA TGG GGA														426
S H N C Y H G E D V G V N C Y G E A N L														153
AGC CAT AAC TGT TAT CAT GGA GAA GAT GTT GGT GTG AAC TGT TAT TAT GGT GAA GCC AAT CTG														486

Fig. 2A



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G	L	R	L	V	D	G	N	N	S	C	S	G	R	V	E	V	K	F	Q	173
GGT	TTG	AGG	CTA	GTG	GAT	GGA	AAC	AAC	TCC	TGT	TCA	GGG	AGA	GTG	GAG	GTG	AAA	TTC	CAA	546
E	R	W	G	T	I	C	D	D	G	W	N	L	N	T	A	A	V	V	C	193
GAA	AGG	TGG	GGG	ACT	ATA	TGT	GAT	GAT	GGG	TGG	AAC	TTG	AAT	ACT	GCT	GCC	GTG	GTG	TGC	606
R	Q	L	G	C	P	S	S	F	I	S	S	G	V	V	N	S	P	A	V	213
AGG	CAA	CTA	GGA	TGT	CCA	TCT	TCT	TTT	ATT	TCT	TCT	GGA	GTT	GTT	AAT	AGC	CCT	GCT	GTA	666
L	R	P	I	W	L	D	D	I	L	C	Q	G	N	E	L	A	L	W	N	233
TTG	CGC	CCC	ATT	TGG	CTG	GAT	GAC	ATT	TTA	TGC	CAG	GGG	AAT	GAG	TTG	GCA	CTC	TGG	AAT	726
C	R	H	R	G	W	G	N	H	D	C	S	H	N	E	D	V	T	L	T	253
TGC	AGA	CAT	CGT	GGA	TGG	GGA	AAT	CAT	GAC	TGC	AGT	CAC	AAT	GAG	GAT	GTC	ACA	TTA	ACT	786
C	Y	D	S	S	D	L	E	L	R	L	V	G	G	T	N	R	C	M	G	273
TGT	TAT	GAT	AGT	AGT	GAT	CTT	GAA	CTA	AGG	CTT	GTA	GGT	GGA	ACT	AAC	CGC	TGT	ATG	GGG	846
R	V	E	L	K	I	Q	G	R	W	G	T	V	C	H	H	K	W	N	N	293
AGA	GTA	GAG	CTG	AAA	ATC	CAA	GGA	AGG	TGG	GGG	ACC	GTA	TGC	CAC	CAT	AAG	TGG	AAC	AAT	906
A	A	A	D	V	V	C	K	Q	L	G	C	G	T	A	L	H	F	A	G	313
GCT	GCA	GCT	GAT	GTC	GTA	TGC	AAG	CAG	TTG	GGA	TGT	GGA	ACC	GCA	CTT	CAC	TTC	GCT	GGC	966
L	P	H	L	Q	S	G	S	D	V	V	W	L	D	G	V	S	C	S	G	333
TTG	CCT	CAT	TTG	CAG	TCA	GGG	TCT	GAT	GTT	GTA	TGG	CTT	GAT	GGT	GTC	TCC	TGC	TCC	GGT	1026

Fig. 2B

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N	E	S	F	L	W	D	C	R	H	S	G	T	V	N	F	D	C	L	H	353
AAT	GAA	TCT	TTT	CTT	TGG	GAC	TGC	AGA	CAT	TCC	GGA	ACC	GTC	AAT	TTT	GAC	TGT	CTT	CAT	1086
Q	N	D	V	S	V	I	C	S	D	G	A	D	L	E	L	R	L	A	D	373
CAA	AAC	GAT	GTG	TCT	GTG	ATC	TGC	TCA	GAT	GGA	GCA	GAT	TTG	GAA	CTG	CGA	CTA	GCA	GAT	1146
G	S	N	N	C	S	G	R	V	E	V	R	I	H	E	Q	W	T	I	I	393
GGA	AGT	AAC	AAT	TGT	TCA	GGG	AGA	GTA	GAG	GTG	AGA	ATT	CAT	GAA	CAG	TGG	TGG	ACA	ATA	1206
C	D	Q	N	W	K	N	E	Q	A	L	V	V	C	K	Q	L	G	C	P	413
TGT	GAC	CAG	AAC	TGG	AAG	AAT	GAA	CAA	GCC	CTT	GTG	GTT	TGT	AAG	CAG	CTA	GGA	TGT	CCG	1266
F	S	V	F	G	S	R	R	A	K	P	S	N	E	A	R	D	I	W	I	433
TTC	AGC	GTC	TTT	GGC	AGT	CGT	CGT	GCT	AAA	CCT	AGT	AAT	GAA	GCT	AGA	GAC	ATT	TGG	ATA	1326
N	S	I	S	C	T	G	N	E	S	A	L	W	D	C	T	Y	D	G	K	453
AAC	AGC	ATA	TCT	TGC	ACT	GGG	AAT	GAG	TCA	GCT	CTC	TGG	GAC	TGC	ACA	TAT	GAT	GGA	AAA	1386
A	K	R	T	C	F	R	R	S	D	A	G	V	I	C	S	D	K	A	D	473
GCA	AAG	CGA	ACA	TGC	TTC	CGA	AGA	TCA	GAT	GCT	GGA	GTA	ATT	TGT	TCT	GAT	AAG	GCA	GAT	1446
L	D	L	R	L	V	G	A	H	S	P	C	Y	G	R	L	E	V	K	Y	493
CTG	GAC	CTA	AGG	CTT	GTC	GGG	GCT	CAT	AGC	CCC	TGT	TAT	GGG	AGA	TTG	GAG	GTG	AAA	TAC	1506
Q	G	E	W	G	T	V	C	H	D	R	W	S	T	R	N	A	A	V	V	513
CAA	GGA	GAG	TGG	GGG	ACT	GTG	TGT	CAT	GAC	AGA	TGG	AGC	ACA	AGG	AAT	GCA	GCT	GTT	GTG	1566

Fig. 2C

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C   K   Q   L   G   C   G   G   G   A   A   G   C   C   T   A   T   G   C   A   T   H   V   F   G   M   T   Y   F   K   E   533
TGT AAA CAA TTG GGA TGT GGA AAG CCT ATG CAT GTG TTT GGT ATG ACC TAT TTT AAA GAA GAA 1626

A   S   G   P   I   W   L   D   D   V   S   C   I   G   N   E   S   S   N   I   W   553
GCA TCA GGA CCT ATT TGG CTG GAT GAC GTT TCT TGC ATT GGA AAT GAG TCA AAT ATC TGG TGG 1686

D   C   E   H   S   G   W   G   G   A   A   G   C   A   T   A   A   T   T   G   T   G   T   A   C   A   G   A   G   A   G   A   T   T   G   T   A   1746
GAC TGT GAA CAC AGT GGA TGG GGA AAG CAT AAT TGT GTA CAC AGA GAG GAT GTG ATT GTA 1746

T   C   S   G   D   A   T   W   G   L   R   L   V   G   G   G   G   G   A   A   C   A   A   C   A   A   C   R   C   S   593
ACC TGC TCA GGT GAT GCA ACA TGG GGC CTG AGG CTG GTG GGC GGC AGC AAC AAC CGC TGC TCG 1806

G   R   L   E   V   Y   F   Q   G   R   W   G   T   V   C   D   D   D   G   W   N   613
GGA AGA CTG GAG GTG TAC TTT CAA GGA CGG TGG GGC ACA GTG TGT GAT GAC GGC TGG AAC 1866

S   K   A   A   A   V   V   C   S   Q   L   D   C   P   S   S   I   I   G   M   633
AGT AAA GCT GCA GCT GTG GTG TGT AGC CAG CTG GAC TGC CCA TCT TCT ATC ATT GGC ATG 1926

G   L   G   N   A   S   T   G   Y   G   K   I   W   L   D   D   V   S   C   D   653
GGT CTG GGA AAC GCT TCT ACA GGA TAT GGA AAA ATT TGG CTC GAT GAT GTT TCC TGT GAT 1986

G   D   E   S   D   L   W   S   C   R   N   S   G   W   G   N   N   D   C   S   673
GGA GAT GAG TCA GAT CTC TGG TCA TGC AGG AAC AGT GGG TGG GGA AAT AAT GAC TGC AGT 2046

H   S   E   D   V   G   V   I   C   S   D   A   S   D   M   E   L   R   L   V   693
CAC AGT GAA GAT GTT GGA GTG ATC TGT TCT GAT GCA TCG GAT ATG GAG CTG AGG CTT GTG 2106
    
```

Fig. 2D

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G G S S R C A G K V E V N V Q G A V G I 713  
 GGT GGA AGC AGC AGG TGT GCT GGA AAA GTT GAG GTG AAT GTC CAG GGT GCC GTG GGA ATT 2166  
  
 L C A N G W G M N I A E V V C R Q L E C 733  
 CTG TGT GCT AAT GGC TGG GGA ATG AAC ATT GCT GAA GTT GTT TGC AGG CAA CTT GAA TGT 2226  
  
 G S A I R V S R E P H F T E R T L H I L 753  
 GGG TCT GCA ATC AGG GTC TCC AGA GAG CCT CAT TTC ACA GAA AGA ACA TTA CAC ATC TTA 2286  
  
 M S N S G C T G G E A S L W D C I R W E 773  
 ATG TCG AAT TCT GGC TGC ACT GGA GGG GAA GCC TCT TCT TGG GAT TGT ATA CGA TGG GAG 2346  
  
 W K Q T A C H L N M E A S L I C S A H R 793  
 TGG AAA CAG ACT GCG GTT GGA TTA AAT ATG GAA GCA AGT TTG ATC TGC TCA GCC CAC AGG 2406  
  
 Q P R L V G A D M P C S G R V E V K H A 813  
 CAG CCC AGG CTG GTT GGA GCT GAT ATG CCC TGC TCT TCT GGA CGT GTT GAA GTG AAA CAT GCA 2466  
  
 D T W R S V C D S D F S L H A A N V L C 833  
 GAC ACA TGG CGC TCT GTC TGT GAT TCT GAT TCT TCT TCT TCT CAT GCT GCC AAT AAT GTG CTG TGC 2526  
  
 R E L N C G D A I S L S V G D H F G K G 853  
 AGA GAA TTA AAT TGT GGA GAT GCC ATA TCT TCT CTT TCT TCT GGA GAT CAC TTT GGA AAA GGG 2586  
  
 N G L T W A E K F Q C E G S E T H L A L 873  
 AAT GGT CTA ACT TGG GCC GAA AAG TTC CAG TGT GAA GGG AGT GAA ACT CAC CTT GCA TTA 2646

Fig. 2E

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C	P	I	V	Q	H	P	E	D	T	C	I	H	S	R	E	V	G	V	V	893
TGC	CCC	ATT	GTT	CAA	CAT	CCG	GAA	GAC	ACT	TGT	ATC	CAC	AGC	AGA	GAA	GTT	GGA	GTT	GTC	2706
C	S	R	Y	T	D	V	R	L	V	N	G	K	S	Q	C	D	G	Q	V	913
TGT	TCC	CGA	TAT	ACA	GAT	GTC	CGA	CTT	GTG	AAT	GGC	AAA	TCC	CAG	TGT	GAC	GGG	CAA	GTG	2766
E	I	N	V	L	G	H	W	G	S	L	C	D	T	H	W	D	P	E	D	933
GAG	ATC	AAC	GTG	CTT	GGA	CAC	TGG	GGC	TCA	CTG	TGT	GAC	ACC	CAC	TGG	GAC	CCA	GAA	GAT	2826
A	R	V	L	C	R	Q	L	S	C	G	T	A	L	S	T	T	G	G	K	953
GCC	CGT	GTT	CTA	TGC	AGA	CAG	CTC	AGC	TGT	GGG	ACT	GCT	CTC	TCA	ACC	ACA	GGA	GGA	AAA	2886
Y	I	G	E	R	S	V	R	V	W	G	H	R	F	H	C	L	G	N	E	973
TAT	ATT	GGA	GAA	AGA	AGT	GTT	CGT	GTG	TGG	GGA	CAC	AGG	TTT	CAT	TGC	TTA	GGG	AAT	GAG	2946
S	L	L	D	N	C	Q	M	T	V	L	G	A	P	P	C	I	H	G	N	993
TCA	CTT	CTG	GAT	AAC	TGT	CAA	ATG	ACA	GTT	CTT	GGA	CAC	CCT	CCC	TGT	ATC	CAT	GGA	AAT	3006
T	V	S	V	I	C	T	G	S	L	T	Q	P	L	F	P	C	L	A	N	1013
ACT	GTC	TCT	GTG	ATC	TGC	ACA	GGA	AGC	CTG	ACC	CAG	CCA	CTG	TTT	CCA	TGC	CTC	GCA	AAT	3066
V	S	D	P	Y	L	S	A	V	P	E	G	S	A	L	I	C	L	E	D	1033
GTA	TCT	GAC	CCA	TAT	TTG	TCT	GCA	GTT	CCA	GAG	GGC	AGT	GCT	TTG	ATC	TGC	TTA	GAG	GAC	3126
K	R	L	R	L	V	D	G	D	S	R	C	A	G	R	V	E	I	Y	H	1053
AAA	CGG	CTC	CGC	CTA	GTG	GAT	GGG	GAC	AGC	CGC	TGT	GCC	GGG	AGA	GTA	GAG	ATC	TAT	CAC	3186

Fig. 2F

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D	G	F	W	G	T	I	C	D	D	G	W	D	L	S	D	A	H	V	V	1073
GAC	GGC	TTC	TGG	GGC	ACC	ATC	TGT	GAT	GAC	GGC	TGG	GAC	CTG	AGC	GAT	GCC	CAC	GTG	GTG	3246
C	Q	K	L	G	C	G	V	A	F	N	A	T	V	S	A	H	F	G	E	1093
TGT	CAA	AAG	CTG	GGC	TGT	GGA	GTG	GCC	TTC	AAT	GCC	ACG	GTC	TCT	GCT	CAC	TTT	GGG	GAG	3306
G	S	G	P	I	W	L	D	D	L	N	C	T	G	T	E	S	H	L	W	1113
GGG	TCA	GGG	CCC	ATC	TGG	CTG	GAT	GAC	CTG	AAC	TGC	ACA	GGA	ACG	GAG	TCC	CAC	TTG	TGG	3366
Q	C	P	S	R	G	W	G	Q	H	D	C	R	H	K	E	D	A	G	V	1133
CAG	TGC	CCT	TCC	CGC	GGC	TGG	GGG	CAG	CAC	GAC	TGC	AGG	CAC	AAG	GAG	GAC	GCA	GGG	GTC	3426
I	C	S	E	F	T	A	L	R	L	Y	S	E	T	E	T	E	S	C	A	1153
ATC	TGC	TCA	GAA	TTC	ACA	GCC	TTG	AGG	CTC	TAC	AGT	GAA	ACT	GAA	ACA	GAG	AGC	TGT	GCT	3486
G	R	L	E	V	F	Y	N	G	T	W	G	S	V	G	R	R	N	I	T	1173
GGG	AGA	TTG	GAA	GTC	TTC	TAT	AAC	GGG	ACC	TGG	GGC	AGC	GTC	GGC	AGG	AGG	AAC	ATC	ACC	3546
T	A	I	A	G	I	V	C	R	Q	L	G	C	G	E	N	G	V	V	S	1193
ACA	GCC	ATA	GCA	GGC	ATT	GTG	TGC	AGG	CAG	CTG	GGC	TGT	GGG	GAG	AAT	GGA	GTT	GTC	AGC	3606
L	A	P	L	S	K	T	G	S	G	F	M	W	V	D	I	Q	C	C	P	1213
CTC	GCC	CCT	TTA	TCT	AAG	ACA	GGC	TCT	GGT	TTC	ATG	TGG	GTG	GAT	GAC	ATT	CAG	TGT	CCT	3666
K	T	H	I	S	I	W	Q	C	L	S	A	P	W	E	R	R	I	S	S	1233
AAA	ACG	CAT	ATC	TCC	ATA	TGG	CAG	TGC	CTG	TCT	GCC	CCA	TGG	GAG	CGA	AGA	ATC	TCC	AGC	3726

Fig. 2G

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P   A   E   E   T   W   I   T   C   E   D   R   I   R   V   R   G   G   D   T   1253
CCA GCA GAA GAG ACC TGG ATC ACA TGT GAA GAT AGA ATA AGA GTG CGT GGA GGA ACC 3786

E   C   S   G   R   V   E   I   W   H   A   G   S   W   G   T   V   C   D   D   1273
GAG TGC TCT GGG AGA GTG GAG ATC TGG CAC GCA GGC TCC TGG GGC ACA GTG TGT GAT GAC 3846

S   W   D   L   A   E   A   E   V   V   C   Q   Q   L   G   C   G   S   A   L   1293
TCC TGG GAC CTG GCC GAG GCG GAA GTG GTG TGT CAG CAG CTG GGC TGT GGC TCT CTG 3906

A   A   L   R   D   A   S   F   G   Q   G   T   G   T   I   W   L   D   D   M   1313
GCT GCC CTG AGG GAC GCT TCG TTT GGC CAG GGA ACT GGA ACC ATC TGG TTG GAT GAC ATG 3966

R   C   K   G   N   E   S   F   L   W   D   C   H   A   K   P   W   G   Q   S   1333
CGG TGC AAA GGA AAT GAG TCA TTT CTA TGG GAC TGT CAC GCC AAA CCC TGG GGA CAG AGT 4026

D   C   G   H   K   E   D   A   G   V   R   C   S   G   Q   S   L   K   S   L   1353
GAC TGT GGA CAC AAG GAA GAT GCT GGC GTG AGG TGC TCT GGA CAG TCG CTG AAA TCA CTG 4086

N   A   S   S   G   H   L   A   L   I   L   S   S   I   F   G   L   L   L   1373
AAT GCC TCC TCA GGT CAT TTA GCA CTT ATT TTA TCC AGT ATC TTT GGG CTC CTT CTC CTG 4146

V   L   F   I   L   L   T   W   C   R   V   Q   K   Q   K   H   L   P   L   1393
GTT CTG TTT ATT CTA TTT CTC ACG TGG TGC CGA GTT CAG AAA CAA CAT CTG CCC CTC 4206

R   V   S   T   R   R   R   G   S   L   E   E   N   L   F   H   E   M   E   T   1413
AGA GTT TCA ACC AGA AGG AGG GGT TCT CTC GAG GAG AAT TTA TTC CAT GAG ATG GAG ACC 4266

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Fig. 2H

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C   L   K   R   E   D   P   H   G   T   R   T   S   D   D   T   P   N   H   G   1433
TGC CTC AAG AGA GAG GAC CCA CAT GGG ACA AGA ACC TCA GAT GAC ACC CCC AAC CAT GGT 4326

C   E   D   A   S   D   T   S   L   L   L   G   V   L   P   A   S   E   A   T   K   1453
TGT GAA GAT GCT AGC GAC ACA TCG CTG TTG GGA GTT CTT CCT GCC TCT GAA GCC ACA AAA 4386

*
TGA
1454
4389

CTTTAGACTTCCAGGGCTCACCAGATCAACCTCTAAATATCTTTGAAGGAGACACAACACTTTTAAATGAATAAAGAGGA 4468
AGTCAAGTTGCCCCATGGAAAACTTGTCCAAATAACATTTCTTGAACAATAGGAGAACACAGCTAAATTGATAAAGACTGG 4547
TGATAATAAAAATTGAATTATGTATATCACTGTATAAAAAAAAACGACGCGTGGGTCTG 4626
AC
4628

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Fig. 2I



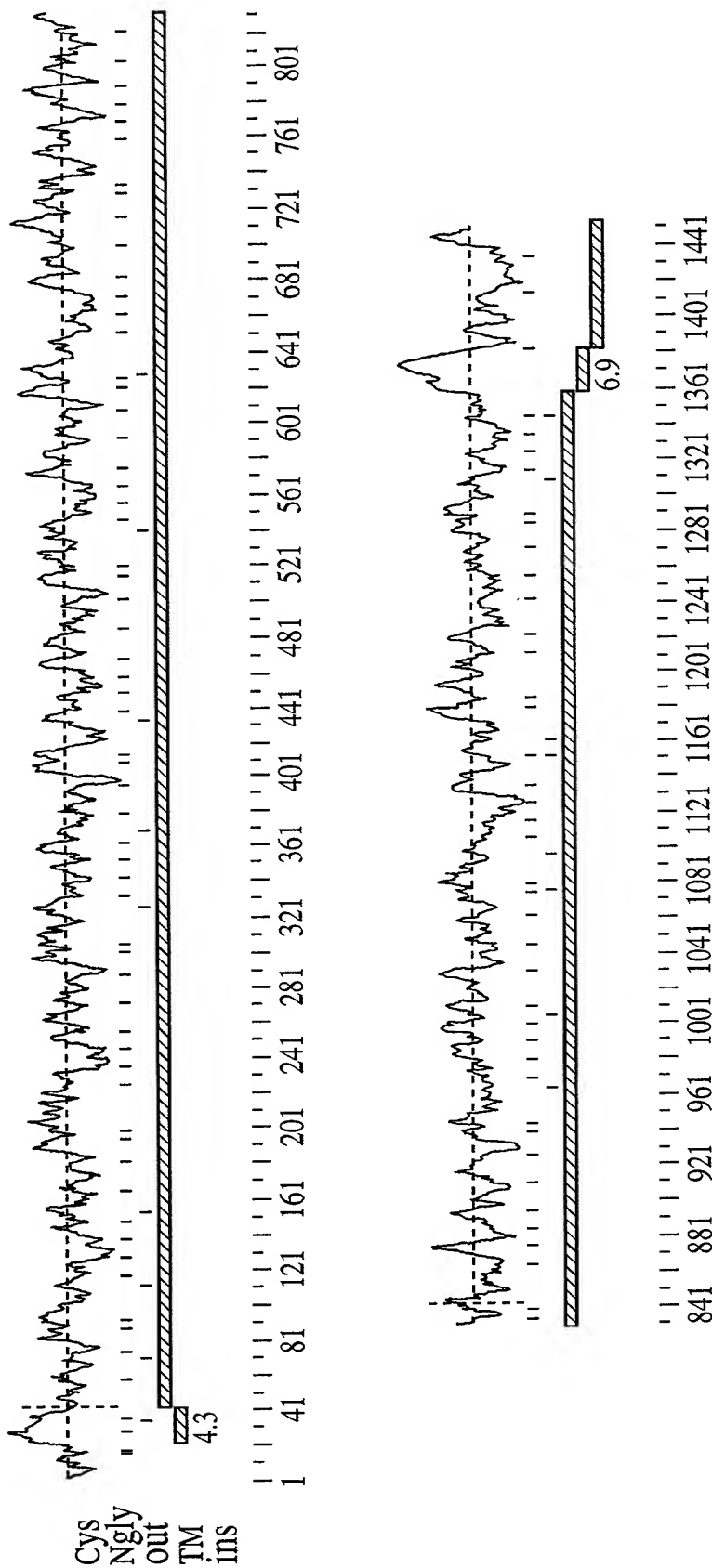


Fig. 2J

Hum.	10	20	30	40	50	60	70
	MMLPQNSWHIDFGRCCCHQNLFSAVVTCILLNSCFLISSFN	GTDL	ELRLVNGD	GPCSGT	VEVKFQ	QGWG	
	:	:	:	:	:	:	:
WC1	MAL-----GR---	HLSLRGL---	CVLL	LLGT--	MVG---	GQALELRLKDG	VHRCEGRVEVKHQGEWG
	10	20	30	40	50		
Hum.	80	90	100	110	120	130	
	TV	CDDGWN	TTASTV	VCKQLG	CFSE	AMFRFG	QAVTR-HGKIWLDDV
	:	:	:	:	:	:	:
WC1	TV	DGYRWT	LK	DA	SV	CRQLGCGAAIG-F	PGGAYFG
	60	70	80	90	100	110	
Hum.	140	150	160	170	180	190	200
	CYHGEDV	GVNCYGEAN	LGLRLVD	GNNSC	SGRVEVKFQ	ERWGTICDDGWN	LNTAAV
	:	:	:	:	:	:	:
WC1	YNHGRDAGV	CSG----	FVRLAGD	GPCSGR	VEVHSGEAWIP	VS	DGNFT
	120	130	140	150	160	170	180
Hum.	210	220	230	240	250	260	270
	VVN	SPAVLRPI	WLDDIL	CQGNELALWNC	RHRGWNHDCSHNED	VT	LTCYDSSD
	:	:	:	:	:	:	:
WC1	HEL	FRESSAQV	WAEEFR	CEGEPELW	VCPRVPC	GGTCHHSGSAQV	VC
	190	200	210	220	230	240	250

**Fig. 2K**

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280      290      300      310      320      330      340
Hum.  LKIQRWGTVCHHKWNNAAADVCKQLGCGTALHFAGLPHLQSGSDVWLDGVSCSGNESFLWDCRHS GT
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  MNISQWRALCASHWSLANANVICRQLGCGVAISTPGGPHLVEEGDQILTARFHCSGAESFLWSCPVTAL
      260      270      280      290      300      310      320

350      360      370      380      390      400      410
Hum.  VNFDC LHQNDVSVICSDGADLELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVKQLGCPFSV
      . :: : : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  GGPDCSHGNTASVICS-GNQI-----QVLPQCND-----SV
      330      340      350

420      430      440      450      460      470      480
Hum.  FGSRRAKPSNEARDIWINISICTGNESALWDCITYDGKAKRTCFRRSDAGVICSDKADLDLRLVGAHSPCY
      :: :: : : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  -----SQPTGSA-----ASEDSA-----PY-----CSDSRQL--RLVDGGGPCA
      360      370      380

490      500      510      520      530      540      550
Hum.  GRLEVKYQGEWGTVCHDRWSTRNAAVVKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCE
      :: :: : : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  GRVEILDQGSWGTICDDGDWLDLDARVVCRQLGCGEALNATGSAHFGAGSGPIWLDNLNCTGKESHVWRCP
      390      400      410      420      430      440      450
```

Fig. 2L

Hum. HSGWGKHNCHREDVIVTCSGDATWGLRLVGGNRCGRLEVFQGRWGTVCDDGWNKAAAVVCSQLDC 560 570 580 590 600 610 620

WC1 SRGWGQHNCRHKQDAGVICS--EFLALRMVSEDQQCAGWLEVFYNGTWGVSVCRNPMEDITVSTICRQLGC 460 470 480 490 500 510 520

Hum. PSSIIIGMGLGNASTGYGKIWLDDVSCDGEDSLWSCRNCGWGNDCSHSEVDGVICSDASDMELRLVGG 630 640 650 660 670 680 690

WC1 GDSGTLNSSVALREGFRPQWVDRIQCRKTDTSWQCPSPDPWYNNSCSPKEEAYIWCADSR--QIRLVDGG 530 540 550 560 570 580 590

Hum. SRCAGKVEVNVQGA VGILCANGWGMNIAEVVCRQLECGSAIRVSREPHTERTLHILMSNSGCTGGEASL 700 710 720 730 740 750 760

WC1 GRCSGRVEILDQGSWGTCDDRWDLDARVVCKQLGCGEALDATVSSFFGTGSGPIWLDEVNCRGEESQV 600 610 620 630 640 650 660

Hum. WDCIRWENKQTACHLNMEASLICS AHRQPRLVGADMPGCSGRVEVKHADTWRSVCDSDFSLHAANVLCREL 770 780 790 800 810 820 830

WC1 WRCPSWGWQRHNCNHQEDAGVICS GF--VRLAGGDGPGCSGRVEVHSGEAWTPVSDGNFTLPTAQVICAEL 670 680 690 700 710 720 730

Fig. 2M

Hum.	840	850	860	870	880	890	900
	NCGDAISLSVGDHFGKGNGLTWAEFQCEGSETHLALCPIVQHPEDTCIHSREVGVCSTRYTDVRLV-NG						
WC1	740	750	760	770	780	790	800
	GCGKAVSVLGHMPFRESQVWAEFRCDGGEPELWSCPRVPCPGTCLHSGAAQVVCVSVYTEVQLMKNG						
Hum.	910	920	930	940	950	960	970
	KSQCDGQVEINVLGHWSGLCDTHWDPEDARVLCRQLSCGTALSTTGKYIGERSVRVWGHFRHCLGNESL						
WC1	810	820	830	840	850	860	870
	TSQCEGQVEMKISGRWRALCASHWSLANANVVCRLGCGVAISTPRGPHLVEGGDQISTAQFHCSGAESF						
Hum.	980	990	1000	1010	1020	1030	1040
	LDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAVPEGSALICLEDKRLRLVDGDSRC						
WC1	880	890	900	910	920	930	940
	LWSCPV TALGGPDCSHGNTASVICSGNHTQVLPQCNDFLSQPAGSAAEESSPYCSDSRQLRLVDGGGPC						
Hum.	1050	1060	1070	1080	1090	1100	1110
	AGRVEIYHDFWGTICDDGWDLSDAHVVQC KLGCGVAFNATVSAHFGEGSGPIWLDDLNC TGETSHLWQC						
WC1	950	960	970	980	990	1000	1010
	GGRVEILDQGSWGTICDDDDWLDDARVVCRQLGCGEALNATGSAHFGAGSGPIWLDDLNC TKGESHVWRC						

Fig. 2N

**Fig. 20**

**Fig. 20**

```

1370      1380      1390      1400      1410
Hum.  LSSIFGLLLVLFILFTWCRVQK-----QKHLPLRVS-----TRRRG-----SLEENLFHEME
      :... :...: . .: :... :... : . . . . . :
WC1  LGSLLFLVILVTQLLRW-RAERRALSSYEDALAEAVYEELDYLLTQKEGLGSPDQMTDVPDENYDDAE
1290      1300      1310      1320      1330      1340      1350

Hum.  TC-----LKRDPHGTRTSD-----DTPNHGCE-----DTSLLG
      . : :...: . . . . . : . . . . . :
WC1  EVPVPGTPSPSQGNEEEVPEKEDGVRSSQTGSLNFSREANPGEGEESFWLLQKKKGAGYDDVELSA
1360      1370      1380      1390      1400      1410      1420

      1450
Hum.  LPASEAT-K
      : . . :
WC1  LGTSPVTF
1430

```

Fig. 2P

**Fig. 2Q-1**



```

280      290      300      310      320      330      340
Hum.  TCTTTCGCCATGTTTCGTTTGGACAAAGCCGTGA--CTAGACATGGAATAATTGGCTTGATGATGTTTC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GCCATTG--GTTTCCCTGGAGGGGCTTATTTGGCCAGGACTTGGCCCATTTGGCTTTTGTATACTTC
220      230      240      250      260      270      280
      350      360      370      380      390      400      410
Hum.  CTGTTATGGAAATGAGTCAGCTCTCTGGGAATGTCAACACCGGGAATGGGGAAGCCATAACTGTTATCAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  ATGTGAAGGACAGAGTCAACTGTCACTGACTGTGAGCAT-TCTAATATTAAGAC-TATC-GTAATGAT
290      300      310      320      330      340      350

420      430      440      450      460      470      480
Hum.  GGAGAAGATGTTGGTGTGAACGTGTTATGGTGAAGCCAA-TCTGGGTTTGAG--GCTAG-TGGATGGAAAC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GGCTATAATCATGGTCGGGA--TGCTGGAGTAGTCTGCTCAGGATTTGTGCGTCTGGCTGGAGGGGATG
360      370      380      390      400      410      420

490      500      510      520      530      540      550
Hum.  AACTCCTGTTCAGGGAGAGTGGAGGTGAAATTCCAAGAAAGGTGGGGACTATATGTGATGATGGGTGGA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GAC-CCTGCTCAGGGCGAGTAGAAGTGCATT--CTGGAGAAGCTTGGATCCCAGTGT-CTGATGGGAACT
430      440      450      460      470      480

```

Fig. 2Q-2

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```

560      570      580      590      600      610      620
Hum.  ACTTGAATACTGCTGCCGTGGTGTGCAGGCAACTAGGATGTCCATCTTCTTTATTTCTTCTGGAGTTGT
      .:. . .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:.
WC1  TCACACTTGCCACTGCC-----CAG-----ATCATCTGT-----GCAGAGTTGGG
490      500      510      520

630      640      650      660      670      680      690
Hum.  TAATAGCCCTGCTGTATTTGCGCCCCCATTTGGCTGGATGACATTTTATGCCAGGGGAATGAGTTGGCACT-
      .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:.
WC1  TTGTGGC-----AAGGCTG--TGTCCTGT-----CCTGGGACATGAG-----CTCTT
530      540      550      560

700      710      720      730      740      750      760
Hum.  CTGGAATTGCAGACATCGTGGATGGGAAATCATGACTGCAGTCACAAATGAGGATGTCACATTAACCTTGT
      .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:.
WC1  CAGAGAGTCCAGT-GCC-----CAGGTCCTG--GGC-----TGAAGAGTTCA-----GG
570      580      590      600

770      780      790      800      810      820      830
Hum.  TATGATAGTAGTGATCTTTGAACCTAAGGCTTGAGGTGGAACCTAACCGCTGTATGGGAGAGTAGAGCTGA
      .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:.
WC1  TGTGAGGGGAGGAGCCCTGAGCT-----CT-----GGGTCTGCCC-CAGAGTG-----CCCTG-
610      620      630      640      650
```

Fig. 2Q-3

Hum.	840	850	860	870	880	890	900
	AAATCCAAGGAAGTGGGGACCGTATGCCACCAATAAGTGAACAATGCTGCAGCTGATGTCGTATGCAA						
	::::	::::	::::	::::	::::	::::	::::
WC1	---TCCA-----GGGGCACGTGT--CACCACA-GTGGATC--TGCT-CAGGTTGTTTGTTCAGCAT	660	670	680	690	700	
Hum.	910	920	930	940	950	960	970
	GCAGTTGGGATGTGGAACCGCACTTCACATTGGCTGGCTTGGCTTCATTTCAGATCAGGGTCTGATGTTGTA						
	::	::	::	::	::	::	::
WC1	ACT-----CAGAAGTCCGGCTCATGACAA-AC-GGCT--CCTC-TCAG-TCAGTGAAGGCAGGTGGAGAT	710	720	730	740	750	760
Hum.	980	990	1000	1010	1020	1030	1040
	TGGCTTGATGGTGTCTCCTGTCTCCGGTAATGAATCTTTCTTTGGACTGCAGACATTCGGAACCGTCA						
	::::	::	::	::	::	::	::
WC1	GAACATT-----TCTG-GACAAATGGAGAGCGCTCTGTGCCTCCC-ACCTGGAGTCTGGCCAATGCC--A	770	780	790	800	810	820
Hum.	1050	1060	1070	1080	1090	1100	1110
	ATTTTGACTGTCTTCAATCAAAACGATGTGTCTGTGATCTGCTCAGATGGAGCAGATTTGGAACCTGCGACT						
	::	::	::	::	::	::	::
WC1	ATGTTATCTGTCAGCTCGGCTGTGGAGTTGCCATCTCCACCCCGGAG-----GACCAC-ACT	830	840	850	860	870	880

**Fig. 2Q-4**

Hum.	1120	1130	1140	1150	1160	1170	1180
	AGCAGATGGAAGTAACAATTGTT	CAGGAGAGTAGAGGTGAGAA	TTCA-TGAACAGTGGTGGACAATATG				
	..	.....	.....	..	.....	.....	..
WC1	TG---GTGGAAGAAG---GTGATCAG--ATCCTAACAGCCCGATTTC	ACTGCTCTG---GGGC----	TG				
	890	900	910	920	930		
Hum.	1190	1200	1210	1220	1230	1240	1250
	TGACCAGAACTGGAAGAAATGAACAAGCCCTTGTGTTTGTAAAGCAGCTAGGATG	TCCGTTTCAGCGTCTTT					
	.....	.....	.....	.....	.....	.....	.....
WC1	AGTCCT-TCCCTGTGGAGTTGT-----CCT-GTGACT-----GCC-CTGGGTG	TCCCTGACTGTTTCCCCAT					
	940	950	960	970	980	990	
Hum.	1260	1270	1280	1290	1300	1310	1320
	GGCAG-TCGTCGTGCTAAACCTAGTAATGAAGCTAGAGACATTTGGATAAACAGCATA	TCTTGCAC	TGGG				
	.....	.....	.....	.....	.....	.....	.....
WC1	GGCAACACAGCCTCTGTGATCTGTCTCAGGAAACAGATCCAGGTGCTTCCC	CAGTGCAACGA-CTCCG--					
	1000	1010	1020	1030	1040	1050	1060
Hum.	1330	1340	1350	1360	1370	1380	1390
	AATGAGTCAGCTCTCTGGGACTGCACATATGATGGA	AAAGCAACATGCTTCCGAAGATCAGATG					
	..	.....	.....	.....	.....	.....	.....
WC1	--TGCTCAACCTACAGGCTCTGC-----GGC-----CTCAGAGGACA-GCGCCC-----CCTACTG						
	1070	1080	1090	1100			

**Fig. 2Q-5**

```

1400      1410      1420      1430      1440      1450      1460
Hum.  CTGAGTAATTGTTCTGATAAGGCAGATCTGGACCTAAGGCTTGTCGGGGCTCATAGCCCCCTGTATGG
      :: ...      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  CTCAGA-----CAG--CAGGCAGCTCCG--CCTGGTG--GACGGGG--GC--GGTCCCTGCGCCGG
1110      1120      1130      1140      1150      1160

1470      1480      1490      1500      1510      1520
Hum.  GAGATTGGAGGTGAAATACCAAGGAGAGTGGGGACTGTGTGTCATGACAGATGGAGCAAGG-AATGC
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  GAGAGTGGAGATCCTTGACCAGGGCTCCTGGGGCACCATCTGTGATGACGGCTGGGAC-CTGGACGATGC
1170      1180      1190      1200      1210      1220

1530      1540      1550      1560      1570      1580      1590
Hum.  A-GCTGTTGTGTAAACAATTGGGATGTGGA-AAGCCTATGCATGTGTTGGTATGACCTATTTAAAG
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  CCGC-GTGGTGTGCAGGCAGCTGGGCTGTGGAGAAGCCCTCA-ATGCCACGGGGTCTGCTCACTTCGGGG
1230      1240      1250      1260      1270      1280      1290

1600      1610      1620      1630      1640      1650      1660
Hum.  AAGCATCAGGACCTATTGCGCTGGATGACGTTTCTTGCAATTGGAATGAGTCAAAATATCTGGGACTGTGA
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  CAGGATCAGGGCCCATCTGTTGGACAACCTGAACCTGCACAGGAAAGGAGTCCACGCTGTGGAGGTGCC
1300      1310      1320      1330      1340      1350      1360
```

Fig. 2Q-6

	1670	1680	1690	1700	1710	1720	1730
Hum.	ACACAGTGGATGGGAAAGCATAATTGTGTACACAGAGAGGATGTGATTGTAACCTGCTCAGGTGATGCA						
.	: :						
WC1	TTCCTGGGGCTGGGGCAGCACAACTGCAGACACAAGCAGACGCCGGGGTTCATCTGCTCAG--AGTTC-						
	1370	1380	1390	1400	1410	1420	1430
	1740	1750	1760	1770	1780	1790	1800
Hum.	ACATGGGGCCCTGAGGCTGGTGGCGGGCAGCAAACCCTGCTCGGGAAGACTGGAGGTGTACTTTCAAGGAC						
.	: :						
WC1	-CT--GGCCCTCAGGATGGTGAGTGAGGACCAGCAGTGTGCTGGGTGGCTGGAAGTTTTCTACAAATGGGA						
	1440	1450	1460	1470	1480	1490	1500
	1810	1820	1830	1840	1850	1860	1870
Hum.	GGTGGGGCACAGTGTGTGATGACGGCTGGAACAGTAAAGCTGCAGCTGTGGTGTAGCCAGCTGGACTG						
.	: :						
WC1	CCTGGGGCAGTGTCTGCCGTAACCCCATGGAAGACATCACTGTGTCCACGATCTGCAGACAGCTTGGCTG						
	1510	1520	1530	1540	1550	1560	1570
	1880	1890	1900	1910	1920	1930	1940
Hum.	CCCATCTTCATCATTTGGCATGGGTCTG-GGAAACGCTTCTA-CAGGATATGAAAAAATTGGCTCGATG						
.	: :						
WC1	T--GGGGACAGTGGAAACCCCTCAACTCTTCTGTGCTCTTAGAGAAGGTTTtagGCCACAGTGGGTGGAT-						
	1580	1590	1600	1610	1620	1630	

**Fig. 2Q-7**

**Fig. 2Q-8**

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```

2230      2240      2250      2260      2270      2280
Hum.  GAGA-GCCTCATTTACAGAA--AGAACATTACACATCTTAATGTCGAATCTGGCTGCACCTGGAGGGGA
      ..  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  CTGTCCTTCCTTCTCGGACGGGATCAGGGCCCATCTGGCTGGATGAAAGTGAAGTGCAGAGGAGAGGA
1910      1920      1930      1940      1950      1960      1970

2290      2300      2310      2320      2330      2340      2350
Hum.  AGCCTCTCTCTGGGATTGTATACGATGGGAGTGGAAACAG-ACTGCGTGTCAATTAATAATGGAAGCAAG
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GTCCCAAGTATGGAGGTGCCCTTCCTGGGGATGGCGGCAACACAAC-TGCAATCATCAAGAAGATGCAGG
1980      1990      2000      2010      2020      2030      2040

2360      2370      2380      2390      2400      2410      2420
Hum.  TTGTATCTGCTCAGCCACAGGACAGCCAGGCTGGTTGGAGCTGATATGCCCTGCTCTGGACGTGTGAA
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  AGTCATCTGCTCAGGATTTGTGC-----GTCTGGCTGGAGGAGATGGACCCCTGCTCAGGGCGGAGTAGAA
2050      2060      2070      2080      2090      2100

2430      2440      2450      2460      2470      2480      2490
Hum.  GTGAAACATGCAGACACATGGCGCTCTGTCTGTGATTCTGTGATTCTCTCTTCAATGCTGCCAATGT--GCT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GTGCATTTCTGGAGAAGCCTGGACCCCAAGTGTCTGATGGAAACTTCACACTCCCACTGCCAGGTCATCT
2110      2120      2130      2140      2150      2160      2170
```

Fig. 2Q-9



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```

2500      2510      2520      2530      2540      2550      2560
Hum.  GTGCAGAGAAATTAATTTGTGGAGATGCCATATCTTCTGTGGGAGATCACTTTGGAAAAGGG-AATGG
      ::::::::::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
2180      2190      2200      2210      2220      2230      2240
WC1  GTGCAGAGC--TGGGATGTGGCAAGGCTGTGTCT-GTCCCTGGGACACATGCCATTTCAGAGAGTCCGATGG
      ::::::::::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

2570      2580      2590      2600      2610      2620      2630
Hum.  TCTAACTTGGGCCGAAAAGTTCCAGTGTGAAGGAGTGAAACTCACCTTGCCATTATGCCCCCATTTGTTCAA
      ::::::::::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
2250      2260      2270      2280      2290      2300      2310
WC1  CCAGGTCCTGGGCTGAAGAGTTCAGGTGTGATGGGGGGGAGCCCTGAGCTCTGGTCCTGCCCCAGAGTGCCC
      ::::::::::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

2640      2650      2660      2670      2680      2690      2700
Hum.  CATCCGGAAGACACTTGTATCCACAGCAGACAGAAAGTTGGAGTTGTCTGTCCCGATATACAGATGTCCGAC
      ::::::::::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
2320      2330      2340      2350      2360      2370      2380
WC1  TGTCCAGGAGGCACATGTCTCCACAGTGGAGCTGCTCAGGTTGTCTGTTCAGTGTACACAGAAAGTCCAGC
      ::::::::::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

2710      2720      2730      2740      2750      2760      2770
Hum.  TTGTGAATGGCAAATCC---CAGTGTGACGGGCAAGTGGAGATCAACGTGCT-TGGACACTGGGGCTCAC
      ::::::::::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
2390      2400      2410      2420      2430      2440      2450
WC1  TTATGAAAAACGGCACCTCTCAATGTGAGGGGCAGGTGGAGAT-GAAGATCTCTGACGATGGAGAGCGC
      ::::::::::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
```

Fig. 2Q-10

	2780	2790	2800	2810	2820	2830	2840
Hum.	TGTGTGACACCCACTGGGACCCAGAAAGATGCCCGTGTTC	TATGCAGACAGCTCAGCTGTGGGACTGCTCT					
	:	:	:	:	:	:	:
WC1	TCTGTGCCCTCCACTGGAGTCTGGCCAAATGCCAAATGTTGTCTGTCTCGTCAGCTCGGCTGTGGAGTCGCCAT						
	2460	2470	2480	2490	2500	2510	2520
	2850	2860	2870	2880	2890	2900	2910
Hum.	CTCAACCACAGGAGGAAAATATATTGGAGAAAGAGTTCGTGTGGGACACAGGTTTCATTGCTTA						
	:	:	:	:	:	:	:
WC1	CTCCACCCCCAGAGGACCACACTTGGTGGAGGAGGTGATCAGATCTCAACAGCCCCAATTTCACCTGCTCA						
	2530	2540	2550	2560	2570	2580	2590
	2920	2930	2940	2950	2960	2970	2980
Hum.	GGGAATGAGTCACCTTCTGGATAAAGTCAAAATGACAGTTCCTGGAGCACCTCCCTGTATCCATGGAAATA						
	:	:	:	:	:	:	:
WC1	GGGCTGAGTCCCTTCCCTGTGGAGTTGTCCCTGTGACTGCCCTTGGGTGGCCTGACTGTTCCCATGGCAACA						
	2600	2610	2620	2630	2640	2650	2660
	2990	3000	3010	3020	3030	3040	3050
Hum.	CTGTCTCTGTGATCTGCACAGGAAGCCTGACCCAGCCACTGTTCCATGCCCTCGCAAAATGTATCTGACCC						
	:	:	:	:	:	:	:
WC1	CAGCCTCTGTGATCTGCTCAGGAAACCACACCCAGGTGCTGCCCCAGTGCAACGACTTCCTGTCTCAACC						
	2670	2680	2690	2700	2710	2720	2730

Fig. 2Q-11

```

3060      3070      3080      3090      3100      3110      3120
Hum.  ATATTGCTGCAGTTCAGAGGGCAGTGCTTTGATCTGCTTAGAGGACAAACGGCTCCGCCCTAGTGGAT
      .      :      :      :      :      :      :      :      :      :      :      :
      :      :      :      :      :      :      :      :      :      :      :      :
WC1   TGCAGGCTCTCGGCCCTCAGAGGAGAGTTCTCCCTACTGCTCAGACAGCAGGACGCTCCGCCCTGGTGGAC
      2740      2750      2760      2770      2780      2790      2800

3130      3140      3150      3160      3170      3180      3190
Hum.  GGGACAGCCGCTGTGCCGGGAGAGTAGAGATCATACAGCGGCTCTGGGCACCATCTGTGATGACG
      :      :      :      :      :      :      :      :      :      :      :      :
      :      :      :      :      :      :      :      :      :      :      :      :
WC1   GGGGGCGGTCCCTGCGGGCGGAGAGTGGAGATCCTTGACCAGGGCTCCTGGGCACCATCTGTGATGATG
      2810      2820      2830      2840      2850      2860      2870

3200      3210      3220      3230      3240      3250      3260
Hum.  GCTGGGACCTGAGCGATGCCACAGTGGTGTGTCAAAAGCTGGGCTGTGGAGTGGCCTTCAATGCCACGGT
      :      :      :      :      :      :      :      :      :      :      :      :
      :      :      :      :      :      :      :      :      :      :      :      :
WC1   ACTGGGACCTGGACGATGCCCGTGTGGTGTGCAGGCAGCTGGGCTGTGGAGAGCCCTCAATGCCACGGG
      2880      2890      2900      2910      2920      2930      2940

3270      3280      3290      3300      3310      3320      3330
Hum.  CTCTGCTCACTTTGGGGAGGGGTCAGGGCCCATCTGGCTGGATGACCTGAACCTGCACAGGAACGGAGTCC
      :      :      :      :      :      :      :      :      :      :      :      :
      :      :      :      :      :      :      :      :      :      :      :      :
WC1   GTCTGCTCACTTCGGGGCAGGATCAGGGGCCCATCTGGCTGGACGACCTGAACCTGCACAGGAACGGAGTCC
      2950      2960      2970      2980      2990      3000      3010
```

Fig. 2Q-12

```

3340      3350      3360      3370      3380      3390      3400
Hum.  CACTTGTGGCAGTGCCCTTCCCGCGGCTGGGGCAGCACGACTGCAGGCACAAGGAGGACGAGGGGTCA
      ::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1   CACGTGTGGAGGTGCCCTTCCCGGGGCTGGGGCGGCACGACTGCAGACACAAGGAGGACGCCGGGGTCA
      3020      3030      3040      3050      3060      3070      3080

3410      3420      3430      3440      3450      3460      3470
Hum.  TCTGCTCAGAAATTCACAGCCCTTGAGGCTCTACAGTGAAACTGAAACAGAGAGCTGTGCTGGGAGATTGGA
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1   TCTGCTCAGAGTTCCTGGCCCTCAGGAT----GGTGAG-CGAGGACCAGCAG-TGTGCTGGGTGGCTGGA
      3090      3100      3110      3120      3130      3140

3480      3490      3500      3510      3520      3530      3540
Hum.  AGTCTTCTATAACGGGACCTGGGGCAGCGTCGGCAGGAGAAACATCACCCACAGCCATAGCAGGCATTGTG
      :: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1   GGTTTTCTACAACGGGACCTGGGGCAGTGTCTGCCGCAGCCCCCATGGAAGATATCACTGTGTCCGTGATC
      3150      3160      3170      3180      3190      3200      3210

3550      3560      3570      3580      3590      3600
Hum.  TGCAGGCAGCTGGGCTGTGGGGAGAAATGGAGTTGTACAGCCTCGCCCTTTA--TCT-AAGACAGGCTCTG
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1   TGCAGACAGCTTGGATGTGGGGACAGTGGA--AGTCT-CAACACCTCTGTGTGCTCTCAGGGAAGGTTCTA
      3220      3230      3240      3250      3260      3270      3280
```

Fig. 2Q-13

**Fig. 2Q-14**

3840	3850	3860	3870	3880	3890	3900
Hum.	GGAAGTGGTGT	CAGCAGCTGGGCTGTGGCTCTGCTCTGGCTGCCCCTGAGGGACGCTTCGTTTGGCCAG				
	.....	.....	.....	.....	.....	.....
WC1	TGAGTGGTGT	CAGCAGCTGGGCTGTGGCTGTGGCCAGGCCCTGGAAGCCGTGCGGTCTGCAGCATTTGGCCCT				
3570	3580	3590	3600	3610	3620	3630
3910	3920	3930	3940	3950	3960	3970
Hum.	GGAAGTGAACCATCTGGTTGGATGACATGCGGTGCAAGAAATGAGTCATTTCTATGGGACTGTCACG					
	.....	.....	.....	.....	.....	.....
WC1	GGAAATGGAGCATCTGGCTGGACGAGGTGCAGTGCGGGGCCCCGGAGTCCTCCCTGTGGGACTGTGTTG					
3640	3650	3660	3670	3680	3690	3700
3980	3990	4000	4010	4020	4030	4040
Hum.	CCAAACCCCTGGGACAGAGTGACTGTGACACAAAGGAAGATGCTGGCGTGAGGTGCTCTGG---ACAGTC					
	.....	.....	.....	.....	.....	.....
WC1	CGGAGCCCCTGGGGCAGAGCGACTGCAAGCACGAGGAGGATGCTGGTGTGAGGTGCTCTGCTGTAAGGAC					
3710	3720	3730	3740	3750	3760	3770
4050	4060					
Hum.	G-----CTGAAATCACTGAATG--CCT-----CCTCAGGT-CATT---TAGCA-CTTATTTATATCCA					
	.....	.....	.....	.....	.....	.....
WC1	AACATTGCCCACGACCACAGCAGGGACCAAGAACCAACCTCAAATTCTCTCCCTGGCATCTTCTCCCTGCCT					
3780	3790	3800	3810	3820	3830	3840

**Fig. 2Q-15**

```

4100      4110      4120      4130      4140
Hum.  G-----TATCTT-----TGGGCTC-CTTCTC-----CTGGTTCT-----GTTATTCFATTTCTCA
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
WC1   GGGGTTCTCTGCCTTATCCTGGGGTCGGCTTCTCTTCCCTGGTCCTCGTCATCCTGGTGACTCAGCTACTCA
3850   3860   3870   3880   3890   3900   3910

      4150      4160      4170      4180
Hum.  CGTGGTG--CCGAGTTCAGAAACAAAAACATCT-----GCCC-----CT-----CAGAGTTT-----
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
WC1   GATGGAGAGCAGAGCGCAGAGCCCTTATCCAGCTATGAAGATGCTCTTGCTGAAGCTGTGTATGAGGAGCT
3920   3930   3940   3950   3960   3970   3980

      4190      4200      4210      4220
Hum.  -----CAAC-----CAGAAGGAGGG--GTTCT-CTCG---AGGAGAAATTATTCATGA-----
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
WC1   CGATTACCTTCTGACACAGAGAAGGAGTCTGGGCAGCCCCAGATCAGATGACTGATGTCCCTGATGAAAAAT
3990   4000   4010   4020   4030   4040   4050

      4230      4240      4250
Hum.  ---GATGGAG-----ACCTG-----CCTC-----AAGAGAGAGGAC
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
WC1   TATGATGATGCTGAAGAAGTACCAGTGCCCTGGAACCTCCTTCTCCCTCTCAGGGGAATGAGGAGGAAGTGC
4060   4070   4080   4090   4100   4110   4120
```

Fig. 2Q-16

```

4260      4270      4280      4290
Hum.  CCACATGGGACAAAGAAC-----CTCAGA-TGACAC---CC-----CCAA-----
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1   CCCCAGAGAAAGGAGGACGGGTGAGGTCTCTCAGACAGGCTCTTTCTGAACTTCTCCAGAGAGGCAGC
4130      4140      4150      4160      4170      4180      4190
Hum.  -----CCATGGTT--GTGAAGA-----TGCTAGCGACAC-----ATCGCTG--TTGGGAGTT
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1   TAATCCCTGGGGAAGGAGAGAGAGCTTCTGGCTGCTCCAGGGGAAGAAAGGGATGCTGGGTATGATGAT
4200      4210      4220      4230      4240      4250      4260
Hum.  CTT-----CCTG-----CCTCTGAAGCCACAAAA
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1   GTTGAACTCAGTGCCCTGGGAACATCCCCAGTGACTTTCTCG
4270      4280      4290      4300
      4310      4320      4330

```

Fig. 2Q-17



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GTCGACCA	CGCTCC	GGTCTG	TGGCTG	AGC	ATG	GCC	CTC	CCA	GCC	CTG	GGC	CTG	L	D	P	W	S	12
																		67
L	L	G	L	F	L	F	Q	L	L	L	L	P	T	T	A	G		32
CTC	CTG	GGC	CTT	TTC	CTC	TTC	CTC	CAA	CTG	CTG	CTG	CCG	ACG	ACG	ACC	GCG	GGG	127
G	G	G	Q	G	P	M	P	R	V	R	Y	A	G	D	E	R	A	52
GGA	GGC	GGG	CAG	GGG	CCC	ATG	ATG	CCC	AGG	GTC	AGA	TAT	GCA	GGG	GAT	GAA	CGT	187
L	S	F	F	H	Q	K	G	L	Q	D	F	D	T	L	L	S	G	72
CTT	AGC	TTC	TTC	CAC	CAG	AAG	GGC	CTC	CAG	GAT	TTT	GAC	ACT	CTG	CTC	CTG	AGT	247
G	N	T	L	Y	V	G	A	R	E	A	I	L	A	L	D	I	Q	92
GGA	AAT	ACT	CTC	TAC	TAC	GTG	GGG	GCT	CGA	GAA	GCC	ATT	CTG	GCC	TTG	GAT	ATC	307
G	V	P	R	L	K	N	M	I	P	W	P	A	S	D	R	K	S	112
GGG	GTC	CCC	AGG	CTA	AAG	AAC	AATG	ATA	CCG	TGG	CCA	GCC	AGT	GAC	AGA	AAA	AAG	367
C	A	F	K	K	K	S	N	E	T	Q	C	F	N	F	I	R	V	132
TGT	GCC	TTT	AAG	AAG	AAG	AGC	AAT	GAG	ACA	CAG	TGT	TTC	AAC	TTC	ATC	CGT	GTC	427
S	Y	N	V	T	H	L	Y	T	C	G	T	F	A	F	S	P	A	152
TCT	TAC	AAT	GTC	ACC	CAT	CTC	TAC	ACC	TGC	GGC	ACC	TTC	GCC	TTC	AGC	CCT	GCT	487
F	I	E	L	Q	D	S	Y	L	L	P	I	S	E	D	K	V	M	172
TTC	ATT	GAA	CTT	CAA	GAT	TCC	TAC	CTG	TTG	CCC	ATC	TCG	GAG	GAC	AAG	GTC	ATG	547

Fig. 3A

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```

K   G   Q   S   P   F   D   P   A   H   K   H   T   A   V   L   V   D   G   M   192
AAA GGC CAA AGC CCC TTT GAC CCC GCT CAC AAG CAT ACG GCT GTC TTG GTG GAT GGG ATG 607

L   Y   S   G   T   M   N   N   F   L   G   S   E   P   I   L   M   R   T   L   212
CTC TAT TCT GGT ACT ATG AAC AAC TTC CTG GGC AGT GAG CCC ATC CTG ATG CGC ACA CTG 667

G   S   Q   P   V   L   K   T   D   N   F   L   R   W   L   H   H   D   A   S   232
GGA TCC CAG CCT GTC CTC AAG ACC GAC AAC TTC CTC CGC TGG CTG CAT CAT GAC GCC TCC 727

F   V   A   A   I   P   S   T   Q   V   V   Y   F   F   F   E   E   T   A   S   252
TTT GTG GCA GCC ATC CCT TCG ACC CAG GTC GTC TAC TTC TTC TTT GAG GAG ACA GCC AGC 787

E   F   D   F   F   E   R   L   H   T   S   R   V   A   R   V   C   K   N   D   272
GAG TTT GAC TTC TTT GAG AGG CTC CAC ACA TCG CGG GTG GCT AGA GTC TGC AAG AAT GAC 847

V   G   G   G   E   K   L   L   Q   K   K   W   T   T   F   L   K   A   Q   L   L   292
GTG GGC GGC GAA AAG CTG CTG CAG AAG AAG TGG ACC ACC TTC CTG AAG GCC CAG CTG CTC 907

C   T   Q   P   G   Q   L   P   F   N   V   I   R   H   A   V   L   L   P   A   312
TGC ACC CAG CCG GGG CAG CTG CCC TTC AAC GTC ATC CGC CAC GCG GTC CTG CTC CCC GCC 967

D   S   P   T   A   P   H   I   Y   A   V   F   T   S   Q   Q   W   Q   V   G   G   332
GAT TCT CCC ACA GCT CCC CAC ATC TAC GCA GTC TTC ACC TTC CAG TGG CAG GTT GGC GGG 1027

T   R   S   S   A   V   C   A   F   S   L   L   D   I   E   R   V   F   K   G   352
ACC AGG AGC TCT GCG GTT TGT GCC TTC TCT CTC TTG GAC ATT GAA CGT GTC TTT AAG GGG 1087

```

Fig. 3B

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K Y K E L N K E T S R W T T Y R G P E T 372  
AAA TAC AAA GAG TTG AAC AAA GAA ACT TCA CGC TGG ACT ACT TAT AGG GGC CCT GAG ACC 1147

N P R P G S C S V G P S S D K A L T F M 392  
AAC CCC CGG CCA GGC AGT TGC TCA GTG GGC CCC TCC TCT GAT AAG GCC CTG ACC TTC ATG 1207

K D H F L M D E Q V V G T P L L V K S G 412  
AAG GAC CAT TTC CTG ATG GAT GAG CAA GTG GTG GGC ACG CCC CTG CTG GTG AAA TCT GGC 1267

V E Y T R L A V E T A Q G L D G H S H L 432  
GTG GAG TAT ACA CGG CTT GCA GTG GAG ACA GCC CAG GGC CTT GAT GGC CAC AGC CAT CTT 1327

V M Y L G T T G S L H K A V V S S G D S 452  
GTC ATG TAC CTG GGA ACC ACC ACA GGG TCG CTC CAC AAG GCT GTG GTA AGT GGG GAC AGC 1387

S A H L V E E I Q L F P D P E P V R N L 472  
AGT GCT CAT CTG GTG GAA GAG ATT CAG CTG TTC CCT GAC CCT GAA CCT GTT CGC AAC CTG 1447

Q L A P T Q G A V F V G F S G G V W R V 492  
CAG CTG GCC CCC ACC CAG GGT GCA GTG TTT GTA GGC TTC TCA GGA GGT GTC GTC TGG AGG GTG 1507

P R A N C S V Y E S C V D C V L A R D P 512  
CCC CGA GCC AAC TGT AGT GTC TAT GAG AGC TGT GTG GAC TGT GTC CTT GCC CGG GAC CCC 1567

H C A W D P E S R T C C L L S A P N L N 532  
CAC TGT GCC TGG GAC CCT GAG TCC CGA ACC TGT TGC CTC CTG TCT TCT GCC CCC AAC CTG AAC 1627

Fig. 3C

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S W K Q D M E R G N P E W A C A S G P M 552  
TCC TGG AAG CAG GAC ATG GAG CGG GGG AAC CCA GAG TGG GCA TGT GCC AGT GGC CCC ATG 1687

S R S L R P Q S R P Q I I K E V L A V P 572  
AGC AGG AGC CTT CGG CCT CAG AGC CGC CCG CAA ATC ATT AAA GAA GTC CTG GCT GTC CCC 1747

N S I L E L P C P H L S A L A S Y Y W S 592  
AAC TCC ATC CTG GAG CTC CCC TGC TCC CAC CTG TCA GCC TTG GCC TCT TAT TAT TGG AGT 1807

H G P A A V P E A S S T V Y N G S L L L 612  
CAT GGC CCA GCA GCA GTC CCA GAA GCC TCT TCC ACT GTC TAC AAT GGC TCC CTC TTG CTG 1867

I V Q D G V G G L Y Q C W A T E N G F S 632  
ATA GTG CAG GAT GGA GTT GGG GGT CTC TAC CAG TGC TGG GCA ACT GAG AAT GGC TTT TCA 1927

Y P V I S Y W V D S Q D Q T L A L D P E 652  
TAC CCT GTG ATC TCC TAC TGG GTG GAC GAC CAG AGC AGC CAG ACC CTG GCC CTG GAT CCT GAA 1987

L A G I P R E H V K V P L T R V S G G A 672  
CTG GCA GGC ATC CCC CGG GAG CAT GTG AAG GTC CCG TTG ACC AGG GTC AGT GGT GGC GCC 2047

A L A A Q Q S Y W P H F V T V T V L F A 692  
GCC CTG GCT GCC CAG CAG TCC TAC TGG CCC CAC TTT GTC ACT GTC CTC TTT GCC 2107

L V L S G A L I I L V A S P L R A L R A 712  
TTA GTG CTT TCA GGA GCC CTC ATC ATC CTC GTG GCC TCC CCA TTG AGA GCA CTC CGG GCT 2167

Fig. 3D

**Fig. 3E**

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Hum.	10	20	30	40	50	60	70
	MALPALGLDPWSLLGLFLFQLQLLLP	TTAGGGGQGPMPRVRYAGDERRALS	FFHQKGLQDFDTLLS				
	.....	.....	.....	.....	.....	.....	.....
Mur.	10	20	30	40	50	60	70
	MALPSLGQDSWSLLRVFFQLFLPSLPPAS	GTGGQGPMPRVKYHAGDGHRA	LSFFQOKGLRDFDTLLS				
	.....	.....	.....	.....	.....	.....	.....
Hum.	80	90	100	110	120	130	140
	GDGNTLYVGAREAILALDIQDPGV	PRLNMI PWPASDRKKSECAFKKS	NETQCFN	FIRVLVS	YNVTHLY		
	.....	.....	.....	.....	.....	.....	.....
Mur.	80	90	100	110	120	130	140
	DDGNTLYVGARETVLALNIQNPGI	PRLNMI PWPASERKKTECAFKKS	NETQCFN	FIRVLVS	YNATHLY		
	.....	.....	.....	.....	.....	.....	.....
Hum.	150	160	170	180	190	200	210
	TCGTFAFSPACTFIELQDSYLLPI	SEDKVMEKGQSPFDP	PAHKHTAVLVDG	MLYSGTMN	NFLGSEPILMR		
	.....	.....	.....	.....	.....	.....	.....
Mur.	150	160	170	180	190	200	210
	ACGTFAFSPACTFIELQDSLLPIL	DKVMDKGQSP	LTFTSTQAVLVDG	MLYSGTMN	NFLGSEPILMR		
	.....	.....	.....	.....	.....	.....	.....
Hum.	220	230	240	250	260	270	280
	TLGSQPVLTNDNFLRWLHHDAS	FVA	IPSTQVVYFFFEET	ASEDFFERL	HTSRVARVCKND	VGGEKLLQ	
	.....	.....	.....	.....	.....	.....	.....
Mur.	220	230	240	250	260	270	280
	TLGSHPVLTNDNFLRWLHHDAS	FVA	IPSTQVVYFFFEET	ASEDFFERL	HTSRVARVCKND	VGGEKLLQ	
	.....	.....	.....	.....	.....	.....	.....

Fig. 3F

Hum.	290	300	310	320	330	340	350
	KKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF						
	::						
Mur.	290	300	310	320	330	340	350
	KKWTTFLKAQLLCAQPGQLPFNIIRHAVLLPADSPSVSRIYAVFTSQWQVGGTRSSAVCAFSLTDIERVF						
	290	300	310	320	330	340	350
Hum.	360	370	380	390	400	410	420
	KGKYKELNKETSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAV						
	::						
Mur.	360	370	380	390	400	410	420
	KGKYKELNKETSRWTTYRGSEVSPRPGSCSMGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAV						
	430	440	450	460	470	480	490
Hum.	ETAQGLDGHSHLVMYLGTGTLHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVW						
	::						
Mur.	430	440	450	460	470	480	490
	ESARGLDGSSHVVMYLGTSGLHKAVVPQDSSAYLVEEIQLSPDSEPVNRNLQLAPAQGAVFAGFSGGIW						
	500	510	520	530	540	550	560
Hum.	RVPRANC SVYESC VDCVLARDPHCAWDPESTRCCLLSAPNLSWKQDMERGNPEWACASGPMRSRLRPQS						
	::						
Mur.	500	510	520	530	540	550	
	RVPRANC SVYESC VDCVLARDPHCAWDPESTRCLLSGST-KPWKQDMERGNPEWVCTRGPMA RSPRRQS						

**Fig. 3G**

[illegible]

**Fig. 3H**



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```
Hum.  GTCG-AC-CC-----ACG-----CGTCCGGT-----CTGTGGCTGAGCATGGC
      : : : :
Mur.  CTCGACGCCCTGGGTTAGGGGCTGTACTGCTGGGGAACCATCTGGTGACCATCTCAGGCTGACCATGGC
      : : : :
Hum.  CCTCCCAGCCCTGGGCCCTGGACCCCTGGAGCCCTCCTGGGCCCTTTTCCCTCTTCCAACTGCTTC-AGCTGCT
      : : : :
Mur.  CCTACCATCCCTGGGCCAGGACTCATGGAGTCTCCTGCGTGTTTTTTCTTCCAACT-CTTCCTGCTGCC
      : : : :
Hum.  GCTGCCGACGACGACCGCGGGGAGCGGGGCGAGGGGCCCATGCCCAGGTCAGATACATATGCAGGGGAT
      : : : :
Mur.  ATCACTGCCACCTGCTTCTGTGGGACTGTGTGTCAGGGGCCCATGCCCAGAGTCAAATACCATGCTGGAGAC
      : : : :
Hum.  GAACGTAGGGCACTTAGCTTCTTCCACCAGAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGTG
      : : : :
Mur.  GGGCACAGGGCCCTCAGCTTCTTCCAAACAAAAGGCCCTCCGAGACTTTTGACACGCTGCTCCTGAGTGACG
```

Fig. 3I

**Fig. 3J**

**Fig. 3K**

[illegible]

**Fig. 3L**

	1090	1100	1110	1120	1130	1140	1150
Hum.	GGGAAATACAAAGAGTTGAACAAGAAACTTCACGCTGGACTACTTATAGGGCCCTGAGACCAACCCCC						
	:::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::						
Mur.	GGGAAGTACAAGGAGCTGAACAAGGAGACCCTCCCGCTGGACCACCTTACCGGGGCTCAGAGGTACGCCCGA						
	1120 1130 1140 1150 1160 1170 1180						
	1160 1170 1180 1190 1200 1210 1220						
Hum.	GGCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGAT						
	:::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::						
Mur.	GGCAGGCAGTTGCTCCATGGGCCCCCTCCTCTGACAAAAGCCTTGACCTTCATGAAGGACCATTTTCTGAT						
	1190 1200 1210 1220 1230 1240 1250						
	1230 1240 1250 1260 1270 1280 1290						
Hum.	GGATGAGCAAGTGGTGGGACGCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGACAGTGGAG						
	:::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::						
Mur.	GGATGAGCACGTGGTAGGAACACCCCCTGCTGGTGAAGTCTGGTGTGGAGTACACACGGCTTGCTGTGGAG						
	1260 1270 1280 1290 1300 1310 1320						
	1300 1310 1320 1330 1340 1350 1360						
Hum.	ACAGCCCAGGGCCTTGATGGGCACAGCCCATCTTGTCA TG TACCTGGGAACCA CCACAGGGTCGCTCCACA						
	::::: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::						
Mur.	TCAGCTCGGGCCTTGATGGGAGCAGCCATGTGGTCA TG TATCTGGGTACCTCCACGGGTCCCCTGCACA						
	1330 1340 1350 1360 1370 1380 1390						

**Fig. 3M**

Hum.	1370	1380	1390	1400	1410	1420	1430
	AGGCTGTGGTAAGTGGGACAGCAGTGCTCATCTGGTGGAGAGATT	CAGCTGTTCCCTGACCCCTGAACC					
Mur.	1400	1410	1420	1430	1440	1450	1460
	AGGCTGTGGTGCCTCAGGACAGCAGTGCTTATCTCGTGGAGGAGATT	CAGCTGAGCCCTGACTCTGAGCC					
Hum.	1440	1450	1460	1470	1480	1490	1500
	TGTTCCGCAACCTGCAGCTGGCCCCACCCAGGTGCAGTGT	TGTAGGCTTCTCAGGAGGTGCTGGAGG					
Mur.	1470	1480	1490	1500	1510	1520	1530
	TGTTCCGAAACCTGCAGCTGGCCCCCGCCAGGTGCAGTGT	TGCAGGCTTCTCTGGAGGCACTCTGGAGA					
Hum.	1510	1520	1530	1540	1550	1560	1570
	GTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGT	GTCTTGCCTTGCCCCGGGACCCCACTGTG					
Mur.	1540	1550	1560	1570	1580	1590	1600
	GTTCCCAAGGCGCAATTGCAGTGTCTACGAGAGCTGTGTGGACTGT	GTGTGCTTGCCAGGGACCCCTCACTGTG					
Hum.	1580	1590	1600	1610	1620	1630	1640
	CCTGGGACCCCTGAGTCCCGAACCTGTTGCCCTCCTGTCTGCCCCCAACCT	GAACTCCTTGAAGCAGGACAT					
Mur.	1610	1620	1630	1640	1650	1660	1670
	CCTGGGACCCCTGAATCAAGACTCTGCAGCCCTTCTGTCTGGCTC-TACCAAGCCT--	TGGAAGCAGGACAT					

Fig. 3N

[illegible]

	1930	1940	1950	1960	1970	1980	1990
Hum.	TCATACCCCTGTGATCTCCTACTGGGTGGACAGCCAGACACCCCTGGCCCTGGATCCTGAAC	TTGGCAG					
	1960	1970	1980	1990	2000	2010	2020
Mur.	TCATACCCCTGTGGTCTCCTATTGGGTAGACAGCCAGACAGCCCTGGCGCTGGACCCCTGAGCTGGCGG						
	2000	2010	2020	2030	2040	2050	2060
Hum.	GCATCCCCCGGAGCATGTGAAGGTCCCGTTGACCAAGGTCAGTGGTGGGCGGCCCTGGCTGCC	CCAGCA					
	2030	2040	2050	2060	2070	2080	2090
Mur.	GCGTTCCCCGTGAGCGTGTGCAGGTCCCGCTGACCAAGGTCGAGGCGGAGCTTCCATGGCTGCC	CCAGCG					
	2070	2080	2090	2100	2110	2120	2130
Hum.	GTCCCTACTGGCCCCACATTTGTCACTGTCACTGTCTCTTGCCTTAGTGCTTTCAGGAGCCCTCAT	CATC					
	2100	2110	2120	2130	2140	2150	2160
Mur.	GTCCTACTGGCCCCCATTTTCTCATCGTTACCGTCCCTCCTGGCCATCGTGCTCCTGGGAGTGCTCACTCTC						
	2140	2150	2160	2170	2180	2190	2200
Hum.	CTCGTGGCCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGTTCAAGGCTGTGAGACCCCTGCGCCCTG						
	2170	2180	2190	2200	2210	2220	2230
Mur.	CTCCTCGCTTCCCCCACTGGGGGCGCTGCGGGCTCGGGGTAAGTTCAAGGCTGTGGGATGCTGCC	CCCCCA					

Fig. 3P



[illegible]

**Fig. 3Q**

```

2490      2500      2510      2520      2530      2540      2550
Hum. ACAGCAGTCTG-CCTCCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur. ACC-CAGTAGGTCCTCCCTGTGGGACTCTCTTCTGC-AAGCACATT-----GGGCT
      2470      2480      2490      2500      2510

      2560      2570      2580      2590      2600      2610
Hum. ACCCCCAGACCTGCTCCTACACTGATA-TTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAG
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      GTCCTCCATACCTGTACTTGTGCTGTGACAGGAAGAGCCAGAC-AGGTTTCTTTGATTTTGATTGACCCAA
      2520      2530      2540      2550      2560      2570      2580

      2620      2630      2640      2650      2660      2670      2680
Hum. GGACCCCT-CCAGAAACACA-GTGTTTCAAGAGATCCTAAAAAACCTGCCCTGTCCCAGGACCCCTATGGTA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur. GAGCCCTGCCCTGTAAACAAACGTGCTCCAGGAGA-CCATGAAAGGTGTGGCTGTCT-GGGATTCTGTGGTG
      2590      2600      2610      2620      2630      2640      2650

      2690      2700      2710      2720      2730      2740      2750
Hum. ATGAACACCAACATCTAAACAATCATATGCTAA-CATGC---CAC--TCCTGGAAACT-CCACTCTGAA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur. ACAAAC-CTAAGCATCCGAGCAAGCTGGGGCTATTCTCTGCAAACTCCATCCCTGAACGCTGTCACTCTAGA
      2660      2670      2680      2690      2700      2710      2720
```

Fig. 3R

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```

2760      2770      2780      2790      2800      2810
Hum.  ----GCTGCCGCTTTGGACACCAACTCCCTTCT-CCCAGG-GTCATGCAGGGATCTGCTCCCTCCTGC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  AGCAGCTGCTGCTTTGAACACACGACCCCTCCTTCCCAAGAGTCTCTATGGAGTTGGC-CCCTTGTGT
2730      2740      2750      2760      2770      2780      2790

2820      2830      2840      2850      2860      2870      2880
Hum.  TTCCCTTACCAGTCGTGCACCGCTGACTCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTCTCTCTTGC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  TTCCCTTACCAGTCGGGCCATACCTGTTT---GGGAAGTCATCTCTGAAGTCTAACCACCTTCCCTTCTTGG
2800      2810      2820      2830      2840      2850

2890      2900      2910      2920      2930      2940      2950
Hum.  TTCAGTTGGGCAGACTCTGATCCCT---TCTGCCCTGGCAGAAATGGCAGGGGTAATCTGAGCCCTTCTTC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  TTCAGTTGGACAGATTGTTATTATTGCTCTCTGCCCTGGCTAGAAATGGGGCATAATCTGAGCCCTTGTTC
2860      2870      2880      2890      2900      2910      2920

2960      2970      2980      2990      3000      3010
Hum.  ACTCCTTTACCC---TAGCTGACCCCTTCACCTCTCCC---CCTCCCTTTTCCCTTTTGGGATTCAGA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  ---CCTTGTCAGTGTGGCTGACCC-TTGACCTCTTCCCTTCCCTCC---TCCCTTTGTTTGGGATTCAGA
2930      2940      2950      2960      2970      2980      2990
```

Fig. 3S

```

3020      3030      3040      3050      3060      3070      3080
Hum.  AAAC TGCTGTCAGAGACTGTTTATTTTATTAAATAATAAGGCTTAAAAAATAAAAAA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  AAAC TGCTGTCAGAGACAATTTATTTTATTATTAATAA-----AGATATAA
      3000      3010      3020                               3030

3090      3100
Hum.  AAAAAAAGGCGGCCGC

      . . . . .
Mur.  GCTTTAAAG-----
      3040

```

**Fig. 3T**

Fig. 3U

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GTCGACCCACGCGTCCGCGGACGCGTGGGACGGCTCCCGGCTGAGTCTGCCCCCGCCGCGCGGGCGCGAGTC	79
GCGAAGCGCGCCTGCGACCCCGCGGCTCCCGGCGCGCTGGAGAGGACGCGAGGAGCC	152
K V A A L L L G L L L E C T E A K K H C	6
AAG GTG GCG GCG CTG CTC GGG CTG CTC TTG GAG TGC ACA GAA GCC AAA AAG CAT TGC	26
W Y F E G L Y P T Y Y I C R S Y E D C C	212
TGG TAT TTC GAA GGA CTC TAT CCA ACC TAT TAT ATA TGC CGC TCC TAC GAG GAC TGC TGT	46
G S R C C V R A L S I Q R L W Y F W F L	272
GGC TCC AGG TGC TGT GTG CGG GCC CTC TCC ATA CAG AGG CTG TTC TGG TAC TTC TGC CTT	66
L M M G V L F C C G A G G C GGC TTC TTC ATC CGG AGG CGC ATG TAC	332
CTG ATG ATG GGC GTG CTT TTC TGC TGC GGA GCC GGC TTC TTC ATC CGG AGG CGC ATG TAC	86
P P P L I E E P A F N V S Y T R Q P P N	106
CCC CCG CCG CTG ATC GAG GAG CCA GCC TTC AAT GTG TCC TAC ACC AGG CAG CCC CCA AAT	452
P G P G A Q Q P G P P Y Y T D P G G P G	126
CCC GGC CCA GGA GCC CAG CAG CCG GGG CCG CCC TAT TAC ACT GAC CCA GGA GGA CCG GGG	512
M N P V G N S M A M A F Q V P P P N S P Q	146
ATG AAC CCT GTC GGG AAT TCC ATG GCA ATG GCT TTC CAG GTC CCA CCC AAC TCA CCC CAG	572

Fig. 4A

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G S V A C P P P P A Y C N T P P P P Y E 166  
GGG AGT GTG GCC TGC CCG CCC CCT CCA GCC TAC TGC AAC ACG CCT CCG CCC CCG TAC GAA 632

Q V V K A K \*

CAG GTA GTG AAG GCC AAG TAG 173  
653

TGGGGTCCCCACGTGCAAGAGGAGACAGGAGAGGGCCCTTTCCCTGGCCCTTCTGTCTTCTGTTGATGTTCACTTCCAG 732  
GAACGGTCTCGTGGGTGCTAAGGGCAGTTCCTCTGATATCCTCACAGCAAGCACAGCTCTCTTTCAGGCTTTCATGG 811  
AGTACAAATATGAACCTCACACTTTGTCTCTCTGTTGCTTCTGTGACGCAGTCTGTGCTCTCACATGGTAGTGT 890  
GGTGACAGTCCCCGAGGGCTGACGTCTTACGGTGGCGTGACCATCTACAGGAGAGACTGAGAGGAAGAAGGCAG 969  
TGCTGGAGGTGCAGGTGGCAATGTAGAGGGCCAGGCCAGCATCCAGGCAAGCATCCTTCTGCCCGGTAATAATAGG 1048  
AAGCCCCATGCCGGGGCTCAGCCGATGAAGCAGCAGCCAGCTGAGCTGAGCCCCAGCAGGTCTCTGCTCCAGCCTGT 1127  
CCTCTCGTCAGCCTTCTCTCCAGAAAGCTGTTGGAGAGACATTCAGGAGAGCAAGCCCTTGTCTGTCATGTTCTGTCT 1206  
CTGTTCAATATCCTAAAGATAGACTTCTCCTGCACCCAGGAAAGGTAGCACGTGCAGCTCTCACCCGAGGATGGGGC 1285  
CTAGAAATCAGGCTTGCCCTTGAGGCTTGACAGTGATCTGACATCCACTAAGCAAAATTTAATTAATTCATGGGAAATCA 1364  
CTTCCCTGCCCAACTGAGACATTCGCAATTTGTGAGCTCTTGCTGATTTGGAGAAAGGACTGTTACCCATTTTTTG 1443  
GTGTGTTTATGGAAGTGCATGTAGAGCGTCTCTGCCCTTTGAAATCAGACTGGGTGTGTCTTCCCTGGACATCACTGC 1522  
CTCTCCAGGCATTCAGGCCCGGGGTCTCCCTCAGGCAGCTCCAGTGGTGGTCTGAAAGGTGCTTCAAA 1601  
ACGGGGCACATCTGGCTGGGAAGTCACATGGACTCTTCCAGGGAGAGACCCAGCTGAGGCGTCTCTCTGAGGTGT 1680  
GTTGGGTCTAAGCGGGTGTGTGCTGGCTCCAAGGAGGAGAGCTTGTGGGAAAGACAGGAGAACTACTGACTCAAC 1759  
TGCACTGACCATGTTGTCAATAATAGAAATAAAGAAAGAGTGGTCGGAAATGCACATTCCTGGATAGGAATCACAGCTCA 1838  
CCCCAGGATCTCACAGGTAGTCTCCTGAGTAGTTGACGGCTAGCGGGGAGCTAGTTCGCCCGCATAGTTATAGTGTGA 1917  
TGTGTGAACGCTGACCTGTCTGTGTCTAAGAGCTATGCAGCTTAGCTGAGCGGCTAGATTACTAGATGTGCTGTAT 1996  
CACGGGGAATGAGGTGGGGTGCTTATTTTTTAATGAACATAATCAGAGCCCTCTTGAGAAATTTGTTACTCATTTGAACCTGG 2075  
AGCATCAAGACATCTCATGGAAGTGATACGGAGTGATTTGGTGTCCATGCTTTTCACTCTGAGGACATTTAATCGGAG 2154

Fig. 4B

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AACCTCCTGGGAAATTTGTGGAGACACTTGGGAACAAAACAGACACCCCTGGGAATGCAGTTGCAAGCACAGATGCTG 2233  
 CCACCAGTGTCTCTGACCACCCCTGGTGTGACTGCTGACTGCCAGCGTGGTACCTCCCATGCTGCAGGCCCTCCATCTAAA 2312  
 TGAGACAAACAAGCACAAATGTTCACTGTTTACAACCAAGACAACTGCGTGGTCCAAACACTCCTCTTCTCCAGGTCA 2391  
 TTTGTTTGGCAATTTTAAATGCTCTTATTTTGTAAATGAAAAAGCACACTAAGCTGCCCTGGAATCGGGTGCAGCTGA 2470  
 ATAGGCACCCCAAGTCCGTGACTAAATTTTCGTTTGTCTTTTGTATAGCAAAATATGTTAAGAGACAGTGGCTAGG 2549  
 GCTCAACAATTTGTATATCCCATGTTTGTGTGAGACAGAGTTTGTTCCTTGAACCTTGGTTAGAAATTTGCTACTGT 2628  
 GAACGCTGATCCTGCATATGGAAGTCCCACTTTGGTGACATTTCTTGGCCATTCTTGTTCATTTGTGGATGGTGGG 2707  
 TTGTGCCCACTTCCCTGGAGTGAGACAGCTCCTGTGTGTAGAAATTCGCCGAGCGTCCGTGTTTGTAGAGTAACTTGAAG 2786  
 CAGATCTGTGCATGCTTTTCTCTCTGCAACAATTTGGCTCGTTTCTCTTTTGTGTTTGTATAGGATCCTGTTTCTT 2865  
 ATGTGTGCAAAATAAAAATAAATTTGGGCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2944  
 AAAAAAAGGCGCGCGC 2964

Fig. 4C

GTCGACCCACGCTCCGGCCGCGGCTCCTTCTGCGCGCTTCAGCTCGTATCCCCGGAGTCCACCCGCCCGTCCCCGGGGT 79  
 M G R R L 5  
 GCGGACTGGCCCTGAGCTGGCCGTACAGCCCGGCTTCGGACGGTCCCTCGCTGGAGCC ATG GGC CGC CGG CTC 151  
 G R V A A L L L G L L L V E C T E A K K H 25  
 GGC AGG GTG GCG GCG CTG CTG CTC GGG CTG CTA GTG GAG TGC ACT GAG GCC AAA AAA CAT 211

Fig. 4D



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C	W	Y	F	E	G	L	Y	P	T	Y	Y	I	C	R	S	Y	E	D	C	45
TGC	TGG	TAT	TTT	GAA	GGA	CTC	TAT	CCC	ACA	TAC	TAT	ATA	TGC	CGT	TCC	TAT	GAA	GAC	TGC	271
C	G	S	R	C	C	V	R	A	L	S	I	Q	R	L	W	Y	F	W	F	65
TGT	GGC	TCC	AGG	TGC	TGT	GTG	AGG	GCC	CTT	TCC	ATA	CAG	AGG	CTG	TGG	TAT	TTT	TGG	TTC	331
L	L	M	M	G	V	L	F	C	C	G	A	G	F	F	I	R	R	R	M	85
CTG	CTG	ATG	ATG	GGT	GTG	CTG	TTC	TGC	TGT	GGT	GCC	GGT	TTC	TTC	ATT	CGC	CGG	CGC	ATG	391
Y	P	P	P	L	I	E	E	P	T	F	N	V	S	Y	T	R	Q	P	P	105
TAT	CCG	CCA	CCA	CTC	ATT	GAG	GAG	CCC	ACA	TTC	AAT	GTG	TCC	TAT	ACC	AGG	CAG	CCA	CCA	451
N	P	A	P	G	A	Q	Q	M	G	P	P	Y	Y	T	D	P	G	G	P	125
AAT	CCT	GCT	CCA	GGA	GCA	GAG	CAG	CAA	ATG	GGA	CCG	CCA	TAT	TAC	ACC	GAC	CCT	GGA	GGA	511
G	M	N	P	V	G	N	T	M	A	M	A	F	Q	V	Q	P	N	S	P	145
GGG	ATG	AAT	CCT	GTT	GGC	AAT	ACC	ATG	GCT	ATG	GCT	TTC	CAG	GTC	CAG	CCC	AAT	TCA	CCT	571
H	G	G	T	T	Y	P	P	P	P	S	Y	C	N	T	P	P	P	P	Y	165
CAC	GGA	GGC	ACA	ACT	TAC	CCA	CCC	CCT	CCT	TCC	TAC	TGC	AAC	ACG	CCT	CCA	CCC	CCC	TAT	631
E	Q	V	V	K	D	K	*													173
GAA	CAG	GTG	GTG	AAG	GAC	AAG	TAG													655
CAAGATGCTACATCAAAGGCAAGAGGATGGACAGGCCCTTTTGTACCTTCCCATCCTCACCATACTTGCTGATAG																				734

Fig. 4E

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GGTGGTCCAAGGGAAAACTTGGATATTCTCAAAGCAAGCCAGCTCTCTTTCAAGTCTTTTGTGGAGGACATTTGAATC 813  
CACACTGTCTCCTCTGTGCTTCTGTGCTCTCTGAGAGAGTGTGGCAACAGTCCCTGAGGGTT 892  
GATATTCTAGGGTGTCCAGGGTAGATCCCTCGGAGAGAGGCTAAGGGAAAGGAAGGCATAGCCCTGTGTGTAGGGG 971  
CAGATAAAGTGGTCAGGCTGAGATAAGACTCACATGATGCAGTAGTTGGCAGTGAACTTCGAAGAGACACTATCCACCA 1050  
TCCCAGCCCATTTCTCCTAATAAGAGCTGTGGGGCTGTGTTGTTGATGCTCTTTGGTCTCCACTCACATTTTGAAAAATAG 1129  
GCTTTCCTCTGCAGGAAATAGGAAAGACCCAAAGTACATATTGCTTCCACTTAAAAATGAGGGTCAGAAACAGGCCCTCAG 1208  
TTGGACATCTATAGTTAAATAAAGGCCATTAGAGAGGGGAAATCTTTAAGTTAGGGGAAATTTCTCTAAATGGAGACATT 1287  
GCGTTTATGAATCATCGTCTGGCTTTTCTTTAGTGCATGTATTGAAGTGAGGGTGTCTTTGAGATCAGATGGGGAG 1366  
AGTGAACCTCTGCGGGGGTGGGTGTCTCTACTCAGAGGGCTCCAACACCCCTTTTCTTAGGTAGTTCTGTGTGATGGGTT 1445  
TTATGGGCACTATAGAGCTGAGGGGCACATTAGCCCGGTAGTTACATTTGACCCCTTGGAGAGGAAGAGACAGCCAAAG 1524  
AAACTCAGCAAAGCAAGACCAGCATTTGCTGAGTTAGAGCTAGGGTTGTATGTGATCCCAACAGAGATGTGCTGGCCTCA 1603  
GAAGAGGGACGTTTGTGGATAGAGCCGTGAAAACCTACTTAGTTGCACAGATGACATAATCAAAAAGTAGAGAAAAAG 1682  
TGTAGTTAGAGATGCCATTTCCAGGTGAGAAATCAGAGCTCATCCATAGATTACAAAGTAGTGGCTGGAGTTAACAGTA 1761  
TGGAGTTCTTTTCCCTTGGGTAGTTAGTCACGTTGATGTGATTTAAACCCAGGTTGAGACCTTGTGTACTAAGAGCAA 1840  
GGAAGTATAGCTAAGATGCTAGATTATTTATATGATGATGTTGGGAGTGGGCTGCAAGGAAGGGGCTGACATTG 1919  
TAAATGAGAAAAATCAGAGCCATTTGATAAACTGTTACTTGTGGATCAGGCATCCAAAAGTGTCTCTTGTAGTGGACATT 1998  
GAGTATTCTTTACCACCTACAAGACCAGGAGGCATGGTGTCTTCCATTGGGGTATTTATATGAGGTAGAGGTTTCAG 2077  
GAATCGACAGTAGTGTGGGCTTAGTTTAAGGACTGAAAGCATAGGACTGGTAGACAGTTTCAATAGGAAACTGCGG 2156  
GGAAGGAATGGATACCTTTAAAGACAGTTTGTGGATGCAGATGCTGCCACCCCATCATTTGAGCACCCCTTGTGTCTCTGGC 2235  
TTCCTGTCACTGGATCCAGTACCCCTCCATGCTTGGTCCCTTGTTTACATAAGACAAACAAAGCACAAATGTCTGCTGTT 2314  
TACAAATCAAGACGACTACATGGTCCAAACATTTCTCTCTCTTCTATCAGTTGTGGCTTTAACTTCCATTTCTCTCCGTT 2393  
CCTTTTAAAAATCAAGAAGCACAGTCAGAGCTGCCCTGGGATTGCATCAGGGAACGGCTGATCAAGGCATTCAGTGTG 2472  
CATGACTAAATCTTATCTTTTGTATAGCAAAATCCCTTTTAAAGAAACTGAACAAATGCTAAGGCTCAGCAAATTTTATACCT 2551  
CAATGTCTGTGAAGGTAAATTTTGTGTTGCCATTGAGCCCCACATTTGGAATTCCTTCTGACGTCAACACTGACAAATGCCCT 2630  
ATGGAATATGCACCTTCTGGGTATATGTCCCAGCATCCCTTGTCTTATGTTTGGTGAGTAAGGCTCACCCCTTCCAGC 2709

Fig. 4F

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AGCTACTTCTGTGCTGAGGTCCTGTAGAGCCGGGGCTTGGGCACAGACATGAGGCAGACTTGTGCATGCTCTTTC 2788  
TTGGCAACACTTGGCTCATATTTCTTGTCTCTTTGTATAGAGTCCTGTTTCCCTATGTATTTAAAAATAATAAAGTG 2867  
AATTAGTCAAAAAAAAAAAAAAAAAAAAAAGGCGGCCGC 2915

Fig. 4G

Hum.	MRRQPAKVAALLLGLLLECTEAKKHCWYFEGLYPTYIICRSYEDCCGSRCCVRALSIQRLWYFWFLMMG	10	20	30	40	50	60	70
	: . . . . .							
Mur.	MGRRLGRVAALLLGLLVECTEAKKHCWYFEGLYPTYIICRSYEDCCGSRCCVRALSIQRLWYFWFLMMG	10	20	30	40	50	60	70
Hum.	VLFCGAGFFIRRRMYPPLIEEPAFNVSYTRQPPNPGGAQQPGPPYYTDPGGPMNPVGNMAMAFQV	80	90	100	110	120	130	140
	: . . . . .							
Mur.	VLFCGAGFFIRRRMYPPLIEEPTFNVSYTRQPPNPAPGAQQMGPPYYTDPGGPMNPVGNMAMAFQV	80	90	100	110	120	130	140
Hum.	PPNSPQGSVACPPPPAYCNTPPPPYEQVVKAK	150	160	170				
	: . . . . .							
Mur.	QPNSPHGGTTYPPPPSYCNTPPPPYEQVVKDK	150	160	170				

Fig. 4H

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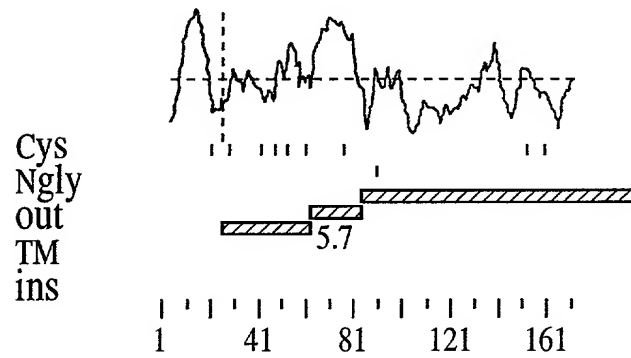


Fig. 4I

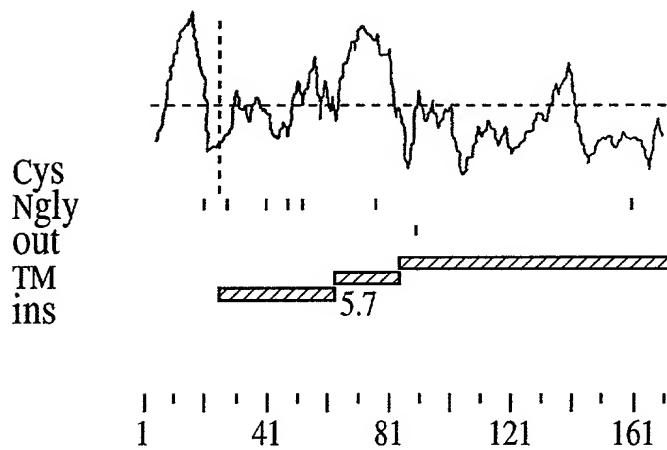


Fig. 4J

**Fig. 5A**

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```

L   C   P   I   I   A   S   E   V   K   A   L   N   A   N   L   S   T   L   E   166
CTC TGT CCC ATT ATT GCA AGT GAA GTC AAA GCG CTA AAT GCC AAC CTC AGC ACA CTG GAG 630

V   L   T   K   I   D   N   Y   T   L   L   D   Y   S   L   I   S   S   P   E   186
GTT TTA ACC AAG ATT GAC AAC TAC ACT CTG CTG GAT TAC TCC CTA ATC AGT TCT CCA GAA 690

I   T   E   N   Y   L   D   L   N   L   K   G   V   F   Y   P   L   E   N   L   206
ATT ACT GAG AAC TAC CTT GAC CTG AAC TTG AAG GGT GTA TTC TAC CCA CTG GAA AAC CTC 750

T   D   P   P   F   S   P   V   P   F   V   L   P   E   R   S   N   S   M   L   226
ACC GAC CCC CCC TTC TCA CCA GTT CCT TTT GTG CTC CCA GAA CGC AGC AAC TCC ATG CTC 810

Y   I   G   I   A   E   Y   F   F   K   S   A   S   F   A   H   F   T   A   G   246
TAC ATT GGA ATC GCC GAG TAT TTC TTT AAA TCT GCG TCC TTT GCT CAT TTC ACA GCT GGG 870

V   F   N   L   T   L   S   T   E   I   S   N   H   F   V   Q   N   S   Q   266
GTT TTC AAT CTC ACT CTC TCC ACC GAA GAG ATT TCC AAC CAT TTT GTT CAA AAC TCT CAA 930

G   L   G   N   V   L   S   R   I   A   E   I   Y   I   L   S   Q   P   F   M   286
GGC CTT GGC AAC GTG CTC TCC CGG ATT GCA GAG ATC TAC ATC TTG TCC CAG CCC TTC ATG 990

V   R   I   M   A   T   E   P   P   I   I   N   L   Q   P   G   N   F   T   L   306
GTG AGG ATC ATG GCC ACA GAG CCT CCC ATA ATC AAT CTA CAA CCA GGC AAT TTC ACC CTG 1050

D   I   P   A   S   I   M   M   L   T   Q   P   K   N   S   T   V   E   T   I   326
GAC ATC CCT GCC TCC ATC ATG ATG CTC ACC CAA CCC AAG AAC TCC ACA GTT GAA ACC ATC 1110

```

Fig. 5B

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V S M D F V A S T S V G L V I L G Q R L 346  
GTT TCC ATG GAC TTC GTT GCT AGT ACC AGT GTT GGC CTG GTT ATT TTG GGA CAA AGA CTG 1170

V C S L S L N R F R L A L P E S N R S N 366  
GTC TGC TCC TTG TCT CTG AAC AGA TTC CGC CTT GCT TTG CCA GAG TCC AAT CGC AGC AAC 1230

I E V L R F E N I L S S I L H F G V L P 386  
ATT GAG GTC TTG AGG TTT GAA AAT ATT CTA TCG TCC ATT CTT CAC TTT GGA GTC CTC CCA 1290

L A N A K L Q Q G F P L P N P H K F L F 406  
CTG GCC AAT GCA AAA TTG CAG CAA GGA TTT CCT CTG CCC AAT CCA CAC AAA TTC TTA TTC 1350

V N S D I E V L E G F L L I S T D L K Y 426  
GTC AAT TCA GAT ATT GAA GTT CTT GAG GGT TTC CTT TTG ATT TCC ACC GAC CTG AAG TAT 1410

E T S S K Q Q P S F H V W E G L N L I S 446  
GAA ACA TCC TCA AAG CAG CAG CCA AGT TTC CAC GTA TGG GAA GGT CTG AAC CTG ATA AGC 1470

R Q W R G K S A P \* 456  
AGA CAG TGG AGG GGG AAG TCA GCC CCT TGA 1500

TTGCCGGTTTGCAATTCACCCCCAGGAAGTAAATGGTCCTTAATCCTACACTACTGTAAACCCAGAAAGGAAAGACAGT 1579  
ACACACTGGAATTGTAAAGCCCTTGTGAATTGCTTAGGCAGAAAGTTTCTTCTTAAGCCCTTCAGGAACCCAGAAATAA 1658  
GGCAGACTCTGTAAAGGGATAAATAGAGGTGTCTGAATGTGAGTGTATGCATGCTGCGTGTCTGTTTATGTTG 1737  
TTTGTTTGTGGGCAAGAAAGATTCTAGGACAAGAGCTAGGCATGTACTTCTGACCAGGTGGGTAAGCAACTCTAAG 1816

Fig. 5C

TCTGTATTGTATTGGTCATTCTCAGTGGAAATCCCTTAGGCCCTCTAGTGGTTTCCCTACCTGCATATTGGTTTC 1895  
ATGTTTATATTCACTGTTACTATCTTCTGTGTTTAAATTGTTTCTATCAAAAAAAAAAAAAAAAAAGGGC 1974  
GGCCGC 1980

Fig. 5D



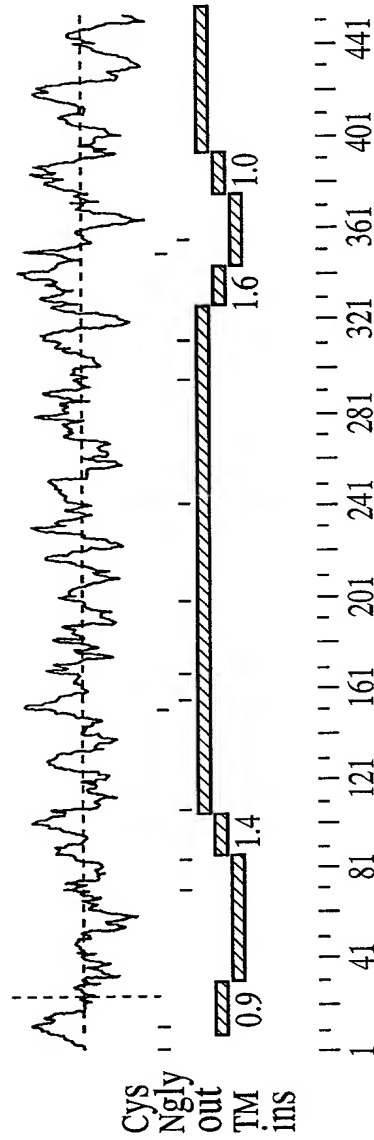


Fig. 5E

```

10      20      30      40      50      60
286 MCTKT-IPVLWGCEL-LWNLVSSSQTIYPGIKARITORALDYGVQAGMKMIEQMLKEKLPDLGSESL
:      :      :      :      :      :      :      :      :      :      :
      :      :      :      :      :      :      :      :      :      :
BPI MARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS--DSF
10      20      30      40      50      60

70      80      90      100     110     120     130
286 EFLKVDYVNYNFSNIKISAFSFPNTSLAFVPGVGIKALTNHGTANISTDWGFESPLFVLYNSFAEPMEE--
:      :      :      :      :      :      :      :      :      :      :
      :      :      :      :      :      :      :      :      :      :
BPI KIKHLGKHYSFYSMDIRFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFLKMSGNFDLSIEGM
70      80      90      100     110     120     130

286 -----KPI-----140     150
:      :      :      :      :      :      :      :      :      :      :
BPI SISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNS
140     150     160     170     180     190     200

286 VKA-LNANLSTLEVLTKIDNYTLLDYSLISSPEITENYLDNLKGVFYFPLENLTDPFPSPFVLPERSN
:      :      :      :      :      :      :      :      :      :      :
      :      :      :      :      :      :      :      :      :      :
BPI VSSKLQPYFQTLPVMTKIDSVAGINYGVLVAPPATTAETLDVQMKGEFYSENHHNPPFPFAPVMEFFPAHD
210     220     230     240     250     260     270
```

Fig. 5F

**Fig. 5G**

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```

10      20      30      40      50      60
286 MCTKTIPVLWGCFLLNLYVSSQTI--YPGIKARITQRALDYGVAQGMKMIQMLKEKKLPDLGSESL
: . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENPGALARAL--PSILLALLTSTPEALGANPGLVARITDKGLQYAAQEGLLALQSELLRITLPDFTG--DL
10      20      30      40      50      60

70      80      90      100     110     120     130
286 EFLKVDYVNFNSNIKISAFSPNTSLAFVPGVGIKALTNHGTANISTDWGFESPLFVLYNSFAEPME--
. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENPRIPHVGRGRYEFHSLNIHEFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFLKMSGNFDLSIEGM
70      80      90      100     110     120     130

286 -----KPI-----LKN-LNEMLCPIIASE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENPSISADLKLGSNPTSGKPTITCSSSCSSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNS
140     150     160     170     180     190     200

160     170     180     190     200     210     220
286 VKA-LNANLSTLEVLTAKIDNYTLDDYSLISSPEITENYLDNLKGVFYPLENLTDPFPSPVFLPERSN
: . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENPVSSKLQPYFQTLPVMTKIDSVAGINYGVLVAPPATTAETLDVQMKGEFYSENHHNPPFPFAPVMEFFPAAHD
210     220     230     240     250     260     270
```

Fig. 5H

[illegible]

**Fig. 51**

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GTCGACCCACGCGTCCGGGAATTGCAGCAGGAAATATGTGAAGAGTTTAAACCACAAAATCTTCTTACTTTAGA	79
ATTAGTTGTTACATTGGCAGGAAAAATAAATGCAGATGTTGGACC ATG TTG GAA ACC TTG TCA AGA CAG	8
W I V S H R M E M W L L I L V A Y M F Q	149
TGG ATT GTC TCA CAC AGA ATG GAA ATG TGG CTT CTG ATT CTG GTG GCG TAT ATG TTC CAG	28
R N V N S V H M P T K A V D P E A F M N	209
AGA AAT GTG AAT TCA GTA CAT ATG CCA ACT AAA GCT GTG GAC CCA GAA GCA TTC ATG AAT	48
I S E I I Q H Q G Y P C E E Y E V A T E	269
ATT AGT GAA ATC ATC CAA CAT CAA GGC TAT CCC TGT GAG GAA TAT GAA GTC GCA ACT GAA	68
D G Y I L S V N R I P R G L V Q P K K T	329
GAT GGG TAT ATC CTT TCT GTT AAC AGG ATT CCT CGA GGC CTA GTG CAA CCT AAG AAG ACA	88
G S R P V V L L Q H G L V G A S N W I	389
GGT TCC AGG CCT GTG GTG TTA CTG CAG CAT GGC CTA GTT GGA GGT GCT AGC AAC TGG ATT	108
S N L P N N S L G F I L A D A G F D V W	449
TCC AAC CTG CCC AAC AAT AGC CTG GGC TTC ATT CTG GCA GAT GCT GGT TTT GAC GTG TGG	128
M G N S R G N A W S R K H K T L S I D Q	509
ATG GGG AAC AGC AGG GGA AAC GCC TGG TCT CGA AAA CAC AAG ACA CTC TCC ATA GAC CAA	148
	569

Fig. 6A

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D	E	F	W	A	F	S	Y	D	E	M	A	R	F	D	L	P	A	V	I	168
GAT	GAG	TTC	TGG	GCT	TTC	AGT	TAT	GAT	GAG	ATG	GCT	AGG	TTT	GAC	CTT	CCT	GCA	GTG	ATA	629
N	F	I	L	Q	K	T	G	Q	E	K	I	Y	Y	V	G	Y	S	Q	G	188
AAC	TTT	ATT	TTG	CAG	AAA	ACG	GGC	CAG	GAA	AAG	ATC	TAT	TAT	GTC	GGC	TAT	TCA	CAG	GGC	689
T	T	M	G	F	I	A	F	S	T	M	P	E	L	A	Q	K	I	K	M	208
ACC	ACC	ATG	GGC	TTT	ATT	GCA	TTT	TCC	ACC	ATG	CCA	GAG	CTG	GCT	CAG	AAA	ATC	AAA	ATG	749
Y	F	A	L	A	P	I	A	T	V	K	H	A	K	S	P	G	T	K	F	228
TAT	TTT	GCT	TTA	GCA	CCC	ATA	GCC	ACT	GTT	AAG	CAT	GCA	AAA	AGC	CCC	GGG	ACC	AAA	TTT	809
L	L	L	P	D	M	M	I	K	G	L	F	G	K	K	E	F	L	Y	Q	248
TTG	TTG	CTG	CCA	GAT	ATG	ATG	ATC	AAG	GGA	TTG	TTT	GGC	AAA	AAA	GAA	TTT	CTG	TAT	CAG	869
T	R	F	L	R	Q	L	V	I	Y	L	C	G	Q	V	I	L	D	Q	I	268
ACC	AGA	TTT	CTC	AGA	CAA	CTT	GTT	ATT	TAC	CTT	TGT	GGC	CAG	GTG	ATT	CTT	GAT	CAG	ATT	929
C	S	N	I	M	L	L	L	G	G	F	N	T	N	N	M	N	M	S	R	288
TGT	AGT	AAT	ATC	ATG	TTA	CTT	CTG	GGT	GGA	TTC	AAC	ACC	AAC	AAT	ATG	AAC	ATG	AGC	CGA	989
A	S	V	Y	A	A	H	T	L	A	G	T	S	V	Q	N	I	L	H	W	308
GCA	AGT	GTA	TAT	GCT	GCC	CAC	ACT	CTT	GCT	GGA	ACA	TCT	GTG	CAA	AAT	ATT	CTA	CAC	TGG	1049
S	Q	A	V	N	S	G	E	L	R	A	F	D	W	G	S	E	T	K	N	328
AGC	CAG	GCA	GTG	AAT	TCT	GGT	GAA	CTC	CGG	GCA	TTT	GAC	TGG	GGG	AGT	GAG	ACC	AAA	AAT	1109

Fig. 6B

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```
L   E   K   C   N   Q   P   T   P   V   R   Y   R   V   R   D   M   T   V   P   348
CTG GAA AAA TGC AAT CAG CCA ACT CCT GTA AGG TAC AGA GTC AGA GAT ATG ACG GTC CCT 1169

T   A   M   W   T   G   G   Q   D   W   L   S   N   P   E   D   V   K   M   L   368
ACA GCA ATG TGG ACA GGA GGT CAG GAC TGG CTT TCA AAT CCA GAA GAC GTG AAA ATG CTG 1229

L   S   E   V   T   N   L   I   Y   H   K   N   I   P   E   W   A   H   V   D   388
CTC TCT GAG GTG ACC AAC CTC ATC TAC CAT AAG AAT ATT CCT GAA TGG GCT CAC GTG GAT 1289

F   I   W   G   L   D   A   P   H   R   M   Y   N   E   I   I   H   L   M   Q   408
TTC ATC TGG GGT TTG GAT GCT CCT CAC CGT ATG TAC AAT GAA ATC ATC CAT CTG ATG CAG 1349

Q   E   E   T   N   L   S   Q   G   R   C   E   A   V   L   *   424
CAG GAG GAG ACC AAC CTT TCC CAG GGA CGG TGT GAG GCC GTA TTG TGA 1397

AGCATCTGACACTGACGATCTTAGGACAACCTCCTGAGGGATGGGCTAGGACCCATGAAGGCAGAAATTACGGAGAGCA 1476
GAGACCTAGTATACATTTTTCAGATTCCCTGCACCTGGCAGCTAAATCCGACACTTACATTTTCTGTATAA 1555
TTAAAGTACTTATTAGGTAAATAGAGGTTTGTATGCTATTATATATATCTACCATCTTGAAGGGTAGGTTTACCTGAT 1634
AGCCAGAAAATATCTAGACATTCTCTATATCATTCAGGTAAATCTCTTTAAACACCTATTGTTTTCTATAAGCCAT 1713
ATTTTGGAGCACTAAAGTAAATGGCAAATTTGGACAGATATTGAGGCTGAGCTGTGGATTATTGTTGACTTTGA 1792
CAAAATAAGCTAGACATTTTCACCTTGTGCCACAGAGACATAACACTACCTCAGGAAGCTGAGCTGCTTTAAGGACAA 1871
CAACAACAAAATCAGTGTACAGTATGATGAAATCTATGTTAAGCATTTCTCAGAAATAAGGCCAAGTTTATAGTTGCA 1950
TCTCAGGGAAGAAAATTTTATAGGATGTTTATGAGTTCTCCAATAAATGCATTCTGCATTACATAAAAAA 2029
AAAAAGGGCGGCCGC 2044
```

Fig. 6C



85 / 95

294 MLETLRQWIVSHRMEMWLLILVAYMFQRNVNSVHMPTKAVDPEAFMNISEIIHQHGYPCEEYEVEDG  
HLP M-----WLL---LTMASLISVLGTTGHLFGKLH---PGSPEVTMNISQMITYWGYPNEEYEVVTEDEG  
10 20 30 40 50 60 70  
20 30 40 50 60 70  
294 YILSVNRIPRGLVQPKKTGSRPVVLLQHGLVGGASNWISNLPNNSLGFILADAGFDVWMGNSRGNASRK  
HLP YILEVNRIPYGKKNSGNTGQRPVFLQHGLLASATNWIISNLPNNSLAFILADAGYDVWLGNRGNTWARR  
60 70 80 90 100 110 120 130 140  
294 HKTSLIDQDEFWAFSYDEMAREFDLPVINFILQKTQEKIYYVGYSGQTMGFIAFSTMPPELAQKIKMYF  
HLP NLYYSPDSVEFWAFSFDDEMAKYDLPATIDFIVKKTGQQLHYVGHSGQTTIGFIAFSTNPSPSLAKRIKTFY  
130 140 150 160 170 180 190  
294 ALAPIATVKHAKSPGTFKFLLPDMMIKGLFGKKEFLYQTRFLRQ-LVIYLCGQVILDQICSNIMLLLGGF  
HLP ALAPVATVKYTKSLINKLRFVPPQSLFKFIFGDKIF-YPHNFFDQFLATEVCSREMLNLLCSNALFIICGF  
200 210 220 230 240 250 260

Fig. 6D

```
280      290      300      310      320      330      340
294 NTNNMMSRASVYAAHTLAGTSVQNILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRVVRDMTVPT
    ....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HLP DSKNFTSRILDVYLSHNPAGTSVQNMFWHTQAVKSGKFQAYDWGSPVQNRMHYDQSQPPYYNVVTAMNVPI
    270      280      290      300      310      320      330

350      360      370      380      390      400      410
294 AMWTGGQDWLSNPDVKMILLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQEEETNLSQGR
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HLP AVWNGGKDLLADPQDVGLLLPKLPNLIYHKEIPFYNHLDFIWAMDAPQEVYNDIVSMISEDKK-----
    340      350      360      370      380      390

420
294 EAVL
HLP -----
```

Fig. 6E

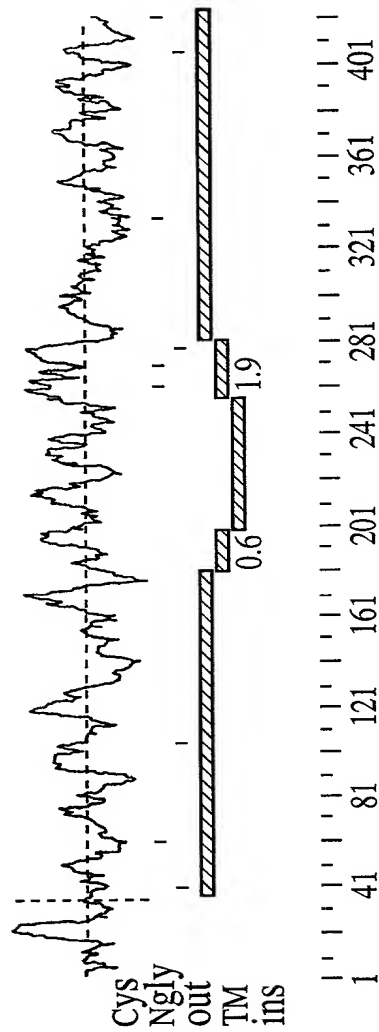


Fig. 6F

```

10      20      30      40      50      60
294 MLETLRQWIVSHRMEMWLLILVAYMFQNVNSVHMPK--AVDPEAFMNISEIIHQHGYPCEEYEVA
:      :      :      :      :      :      :      :      :      :      :
:      :      :      :      :      :      :      :      :      :      :
LAL M-----KMRFLGLVVCIVLWPLHSEGGKLTAVDPETNMNVSEIISYWGFPSSEYLVETE
      10      20      30      40      50

      70      80      90      100     110     120     130
294 DGYILSVNRIPRGLVQPKKTGSRPVVLLQHGLVGGASNWISNLPNNSLGFILADAGFDVWMGNSRGN
:      :      :      :      :      :      :      :      :      :      :
:      :      :      :      :      :      :      :      :      :      :
LAL DGYILCLNRIPHGRKNHSDKGPVVFLOHGLLADSSNWVTNLANSSLGFILADAGFDVWMGNSRGNTWS
      60      70      80      90      100     110     120

      140     150     160     170     180     190     200
294 RKHKTLSIDQDEFWAFSYDEMARFDLPVAVINFILQKTGQEKIYYVGYSGTTMGFIASFSTMPELAQIKM
:      :      :      :      :      :      :      :      :      :      :
:      :      :      :      :      :      :      :      :      :      :
LAL RKHKTLSVSQDEFWAFSYDEMAKYDLPASINFILNKTGQEQVYYVGHSGTTIGFIASFQIPELAKRIKM
      130     140     150     160     170     180     190

      210     220     230     240     250     260     270
294 YFALAPIATVKHAKSPGTFKFLLPDMMIKGLFGKKEFLYQTRFLRQLVIYLCGQVILDQICSNIMLLGG
:      :      :      :      :      :      :      :      :      :      :
:      :      :      :      :      :      :      :      :      :      :
LAL FFALGPVASVAFCTSPMAKLGRLPDHLLIKDLFGDKFELPQSAFLKWLGTHVCHVILKELCGNLCFLLCG
      200     210     220     230     240     250     260
```

Fig. 6G

```

280      290      300      310      320      330      340
294 FNTNNMMSRASVYAAHTLAGTSVQNILHWSQAVNSGELRAFDWGSETKNLEKNQPTPVRYRVRDMTVP
:: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
LAL FNERLNMSRVDVYTTHTSPAGTSVQNNMLHWSQAVKFKQFAFDWGSSAKNYFHYNQSYPTTNNVKDMLVP
270      280      290      300      310      320      330

350      360      370      380      390      400      410
294 TAMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQQEETNLSQGR
:::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
LAL TAVWSGGHDWLADVDVNVNILLTQITNLVFHESIPWEHLDFIWGLDAPWRLYNKIINLMRKYQ-----
340      350      360      370      380      390

420
294 CEAVL

LAL -----

```

Fig. 6H

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GTCGACCCACGGTCCACGGGAGGGCTCCCGGGCGCAGCATTGCCCCCTGCACCACTCAACCAAG ATG GCT 75

T L G H T F P F Y A G P K P T F P M D T 22  
ACT TTG GGA CAC ACA TTC CCC TTC TAT GCT GGC CCC AAG CCA ACC TTC CCG ATG GAC ACC 135

T L A S I I M I F L T A L A T F I V I L 42  
ACT TTG GCC AGC ATC ATG ATC TTT CTG ACT GCA CTG GCC ACG TTC ATC ATC GTC ATC CTG 195

P G I R G K T R L F W L L R V V T S L F 62  
CCT GGC ATT CGG GGA AAG ACG AGG CTG TTC TGG CTG CTT CGG GTG GTG ACC AGC TTA TTC 255

I G A A I L A V N F S S E W S V G Q V S 82  
ATC GGG GCT GCA ATC CTG GCT GCT GTG AAT TTC AGT TCT GAG TGG TCT GTG GGC CAG GTC AGC 315

T N T S Y K A F S S E W I S A D I G L Q 102  
ACC AAC ACA TCA TAC AAG GCC TTC AGT TCT GAG TGG ATC AGC GCT GAT ATT GGG CTG CAG 375

V G L G G V N I T L T G T P V Q Q L N E 122  
GTC GGG CTG GGT GGA GTC AAC ATC ACA CTC ACA GGG ACC CCC GTG CAG CAG CTG AAT GAG 435

T I N Y N E E F T W R L G E N Y A E C 142  
ACC ATC AAT TAC AAC GAG GAG TTC ACC TGG CGC CTG GGT GAG AAC TAT GCT GAG GAG TGT 495

A K A L E K G L P D P V L Y L A E K F T 162  
GCA AAG GCT CTG GAG AAG GGG CTG CCA GAC CCT GTG TTG TAC CTA GCT GAG AAG TTC ACT 555

Fig. 7A

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P	R	S	P	C	G	L	Y	R	Q	Y	R	L	A	G	H	Y	T	S	A	182
CCA	AGA	AGC	CCA	TGT	GGC	CTA	TAC	CGC	CAG	TAC	CGC	CTG	GGG	GGA	CAC	TAC	ACC	TCA	GCC	615
M	L	W	V	A	F	L	C	W	L	L	A	N	V	M	L	S	M	P	V	202
ATG	CTA	TGG	GTG	GCA	TTC	CTC	TGC	TGG	CTG	CTG	GCC	AAT	GTG	ATG	CTC	TCC	ATG	CCT	GTG	675
L	V	Y	G	G	Y	M	L	L	A	T	G	I	F	Q	L	L	A	L	L	222
CTG	GTA	TAT	GGT	GGC	TAC	ATG	CTA	TTG	GCC	ACG	GGC	ATC	TTC	CAG	CTG	TTG	GCT	CTG	CTC	735
F	F	S	M	A	T	S	L	T	S	P	C	P	L	H	L	G	A	S	V	242
TTC	TTC	TCC	ATG	GCC	ACA	TCA	CTC	ACC	TCA	CCC	TGT	CCC	CTG	CAC	CTG	GGC	GCT	TCT	GTG	795
L	H	T	H	H	G	P	A	F	W	I	T	L	T	T	G	L	L	C	V	262
CTG	CAT	ACT	CAC	CAT	GGG	CCT	GCC	TTC	TGG	ATC	ACA	TTG	ACC	ACA	GGA	CTG	CTG	TGT	GTG	855
L	L	G	L	A	M	A	V	A	H	R	M	Q	P	H	R	L	K	A	F	282
CTG	CTG	GGC	CTG	GCT	ATG	GCG	GTG	GCC	CAC	AGG	ATG	CAG	CCT	CAC	AGG	CTG	AAG	GCT	TTC	915
F	N	Q	S	V	D	E	D	P	M	L	E	W	S	P	E	E	G	G	L	302
TTC	AAC	CAG	AGT	GTG	GAT	GAA	GAC	CCC	ATG	CTG	GAG	TGG	AGT	CCT	GAG	GAA	GGT	GGA	CTC	975
L	S	P	R	Y	R	S	M	A	D	S	P	K	S	Q	D	I	P	L	S	322
CTG	AGC	CCC	CGC	TAC	CGG	TCC	ATG	GCT	GAC	AGT	CCC	AAG	TCC	CAG	GAC	ATT	CCC	CTG	TCA	1035
E	A	S	S	T	K	A	Y	C	K	E	A	H	P	K	D	P	D	C	A	342
GAG	GCT	TCC	TCC	ACC	AAG	GCA	TAC	TGT	AAG	GAG	GCA	CAC	CCC	AAA	GAT	CCT	GAT	TGT	GCT	1095

Fig. 7B

L \*  
 TTA TAA  
 344  
 1101  
 1180  
 1259  
 1338  
 1417  
 1496  
 1575  
 1654  
 1733  
 1812  
 1891  
 1970  
 2049  
 2128  
 2133  
 CATTCTCCCCGTGAGGCCACCTGGACTTCAGTCTGGCTCCAAACCTCATTTGGCGCCCCATAAAACCAGCAGAACTG  
 CCTCAGGGTGGCTGTTACAGACACCCAGCACCAATCTACAGACGGAGTAGAAAAAGGAGGCTCTATATACTGATGTT  
 AAAAAACAACAAAAAGCCCTAAGGGACTGAAGAGATGCTGGCCCTGTCCATAAAGCCCTGTTGCCCATGATAAG  
 GCCAAGCAGGGCTAGCTTATCTGCACAGCAACCCAGCCTTTCCTGTGCTGCCCTTCAAGATGCTATTCACTGA  
 AACCTAACTTCAACCCCAATAACACAGCAGGGTGGGGTTACATATGATTCTCCTATGGTTTCCCTCTCATCCCTCGGCA  
 CCTCTTGTTTTCCTTTTCCCTGGGTTCTTGTCTCTCTTACTTCTCCAGCTTGTGTGGCCTTTTGGTACAATGAA  
 AGACAGCACTGGAAAGGAGGGAACCAAACTTCTCATCCCTAGGTCTAACATTAACCAACTATGCCACATCTCTTTGA  
 GCTTCAGTTCCCAAAATTGCTACATAAGATTGCAAGACTTGCAAGACTTGGCAATCTTGGGATTTATCTTCTATGCCCTTGCTGA  
 CACCTACCTTGGCCCTCAACACACCTCACAAAGAGCCAGGTGGGAAGTTAGGGAATCAACTCCAAAAACGCTATTCCT  
 TCCCACCCCACTCAGCTGGGCTAGCTGAGTGGCATCCAGGACGGGGAGTGGTGACCTGCCCTCATCACTGCCACCTAA  
 CGTCCCCCTGGGGTGGTTCAGAAAGATGCTAGCTCTGGTAGGGTCCCTCCGGCCTCACTAGAGGGCGCCCTATTACTC  
 TGGAGTCGACGCAGAGAAATCAGGTTTTCACAGCACTGCGGAGAGTGTACTAGGCTGTCTCCAGCCCAAGCTCATGA  
 GGACGTGCGACCCCGCGGAGAGCCATGAAAATTAATGGGAAAAACAGTTTTAAAAAAGGGCGG  
 GCGGC

Fig. 7C



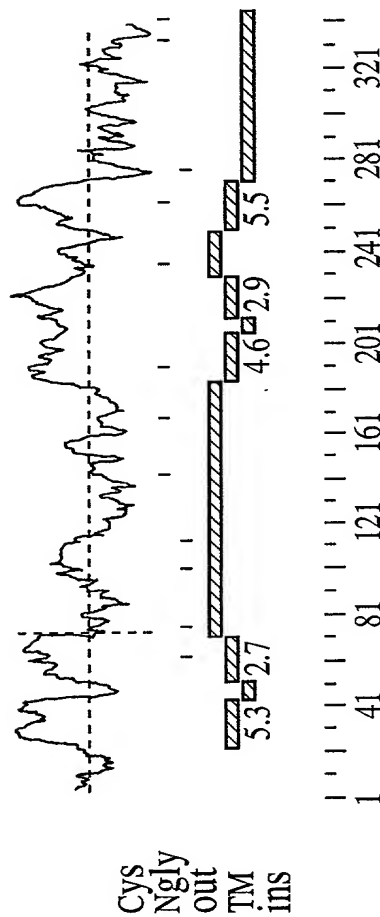


Fig. 7D

```

296 MATLGHFFPYAGPKPTFFPMDTTLASIIMIFLTALATFIVILPGIRGKTRFLWLLRVVTSLFIGAAILAV
: .. :... .. :: ..... :.. : : .....
CRP M-RIAH-----ASSRGNI-----SIFS VF L I P L I A Y I L I L P G V R -R K R V V T T V T V L M L A V G G A L I A S
      10          20        30       40       50       60       70

296 NFSSEWSVGQVSTNTSYKAFSSEWISADIGLVGLGVNITL-----TGTPVQQQLNETIN--YNEEFTW
      80          90         100        110        120        130

CRP LIYPCWASGSQMIYTQFRGHSNERILAKIGVEIGLQKVNVTLKFERLLSSNDVLPGSDMTELYYNEGFDI
      60          70         80         90        100        110        120

296 RLGENYAEECAKALEKGLDPVLYLA EKFT-PRSPCGLYRQYRLAGHYTSAMLVVAFLCWLLANV-MLSM
      140         150         160         170         180         190         200

CRP SGISSMAEALHHGLENGLPYPMLS VLEYFSLNQDSFDWGRHRYRVAGHYTHAAIWFAFACWCLSVVLMLFL
      130         140         150         160         170         180         190

296 PVLVGYGMYLLATGIFQLLALLFFSMATSLTSPCPHLH---GASVLHTHHGP AF----WITLTTGLLCVL
      210         220         230         240         250         260

CRP PHNAYKS--ILATGISCLIA CLVYL----LLSPCELR I A F T G E N F E R V D L T A T F S F C F Y L I F A I G I L C V L
      200         210         220         230         240         250         260

```

**Fig. 7E**

```

296 LGLAMAVAHRMQPHRLKAFFNQSVDEDPMLEW-----SPEEGLLSPRY--RSMADSPKSQDIPLSEAS
      :::: . . :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
CRP CGLGLGICEHWRIYTLSTFLDASLDEHVGPWKKLPTGGPALQGVQIGAYGTNTTNSSRDKNDISSDKTA
      270 280 290 300 310 320 330
296 STKAY-----CK-----EAHPKDPD-----CA---L
      330 340
CRP GSSGFQSRSTCQSSASSALRSQSSIETVHDEAELERTHVHFLQEPCCSSST
      340 350 360 370 380

```

**Fig. 7F**